

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 5, 2001, 12:14:09 : Search time 87.49 Seconds
(without alignments)
1671.014 Million cell updates/sec

Title: US-09-176-664-16
Perfect score: 5722
Sequence: 1 MFOTKLRFNETWEDLPKMSCT.....CIHQSIILTSREILPPSLSK 1105

Scoring table: BLOSUM62
Gapop 10.0 , Gapept 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SPREMBL_16:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mhc:*
8: sp_mammal:*
9: sp_organelle:*
10: sp_phage:*
11: sp_plant:*
12: sp_protent:*
13: sp_unclassified:*
14: sp_vertebrate:*
15: sp_virus:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3717.5	65.0	1112	11	054982 mus musculu
2	2359.5	41.2	1171	6	09T88 oryctolagus
3	2358.5	41.2	1137	13	093569 gallus gall
4	2357.5	41.2	1134	6	028204 bos taurus
5	2357.5	41.2	1151	6	018867 macaca mula
6	2356.5	41.2	1154	4	012921
7	2356.5	41.2	1154	4	09UB80
8	2356.5	41.2	1178	4	012960
9	2356.5	41.2	1178	4	013150
10	2355.5	41.2	1113	4	012917
11	2354.5	41.1	1113	4	09UOK6
12	2354.5	41.1	1171	11	09R196
13	2351.5	41.1	1152	6	018866
14	2350	41.1	1196	6	008460
15	2349.5	41.1	1118	13	098951
16	2349.5	41.1	1137	13	012942
17	2348	41.0	1166	13	073728
18	2347.5	41.0	1163	11	008626
19	2344	41.0	1243	11	055180

20	2338	40.9	1210	11	09WU13
21	2336.5	40.8	1178	11	062976
22	2331.5	40.7	1173	13	073729
23	2331	40.7	1200	13	073731
24	2329.5	40.7	1136	6	046371
25	2327.5	40.7	1231	13	073730
26	2302.5	40.2	1156	6	028265
27	2251	39.3	1144	13	09W7J2
28	2114	36.9	971	11	088659
29	2008.5	35.1	1175	5	09VC51
30	2002.5	35.0	1175	5	024369
31	1995	34.9	1184	5	003720
32	1980	34.6	1236	5	09TWA1
33	1873.5	32.7	985	5	09U268
34	1770.5	30.9	885	4	012791
35	1538.5	26.9	609	4	012886
36	1414	24.7	792	13	013110
37	526.5	9.2	264	13	09PS76
38	515.5	9.0	292	13	09PS77
39	468.5	8.2	1151	4	09P2C5
40	451	7.9	1237	11	092258
41	361	6.3	1119	5	019190
42	316.5	5.5	1017	5	060980
43	270	4.7	1159	5	060981
44	252.5	4.4	1698	5	09V5J8
45	209.5	3.7	455	2	067715

ALIGNMENTS

RESULT	1	PRELIMINARY:	PRT:	1112 AA.
ID	054982			
AC	054982:			
DT	01-JUN-1998 (TREMBLrel. 06, Created)			
DT	01-JUN-1998 (TREMBLrel. 06, Last sequence update)			
DT	01-OCT-2000 (TREMBLrel. 15, Last annotation update)			
DE	POTASSIUM LARGE CONDUCTANCE PH-SENSITIVE CHANNEL, SUBFAMILY M, ALPHA MEMBER 3 (PH-SENSITIVE MAXI K+ CHANNEL).			
DE	MEMBER 3 (PH-SENSITIVE MAXI K+ CHANNEL).			
GN	KCNMA3 OR SLO3.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Schreiber M., Wei A., Yuan A., Gaut J., Saito M., Salkoff L.,			
RL	J. Biol. Chem. 0:0-(1998).			
DR	EMBL: AF039213; AAB9742.1; -.			
DR	MGD: MGI:1202300; Kcnma3.			
DR	InterPro: IPR000636; -.			
DR	InterPro: IPR001622; -.			
DR	Pfam: PF00520; Ion_trans; 1.			
RW	Ionlic Channel.			
SEQ	SEQUENCE 1112 AA; 126157 MW; 2BCECF5386F62115 CRC64;			
Query Match	65.0%; Score 3717.5; DB 11; Length 1112;			
Best Local Similarity	69.0%; Pred. No. 2.9e-258;			
Matches 729; Conservative 119; Mismatches 190; Indels 19; Gaps 5;				
Oy	1 MFOTKLRFNETWEDLPKMSCTFEIOAFLISSVFPEFSGILILIRLIRMSVKKMQIIG 60			09WU13 ratu s norv
Db	1 MSQTLIDSLNOKELRETSCTEIOAFLISSLATTFGGILILIFERIALKSSRSKYYKG 60			062976 ratu s norv
Oy	1 TGIILFTSGTARSVRSIAFOGFRDHIEMLLSAQTFVGQVLIIVFVLSIGSLIY 120			073729 trache m s
Db	61 PGLILEFSRRIEANPLRIKTFHGVFRQREMLLSAQTVGQVLIIVFVLSIGSLIY 120			073731 trache m s
Oy	121 FINSADPVGSGSYEDKTIIPDLVNAFFSFGIRFMAADDKIRFWLEMSIVDIFIP 180			046371 o r y c t o l a g u s
Db	121 FINSMDPVRCSSYEDKTIIVHGLSFAFFSFGIRFMAADDKIRFWLEMSIVDIFIP 180			028265 canis fami l
Oy	121 FINSMDPVRCSSYEDKTIIVHGLSFAFFSFGIRFMAADDKIRFWLEMSIVDIFIP 180			09W7J2 trache m s
Db	121 FINSMDPVRCSSYEDKTIIVHGLSFAFFSFGIRFMAADDKIRFWLEMSIVDIFIP 180			088659 ratu s norv

QY 181 PTFISYLYKSNMGLRFLRALRLLELPQIILRAIKTSNVSFKSLSTILSTWPTAAG 240
DB 181 PTFISYLYKSNMGLRFLRALRLLELPQIILRAIKTSNVSFKSLSTILSTWPTAAG 240
QY 241 FIIHVENSGDPMWLGKRNQNSITFESTIYLVWATTSTVFGDVAKTSLGRTFMEFLGS 300
DB 241 FIIHVENSGDPMWLGKRNQNSITFESTIYLVWATTSTVFGDVAKTSLGRTFMEFLGS 300
QY 301 LIIFANIPPEKVELFANKRKRTSSYEALEKGFIVCGNITVDSVTAFLRFLRDLKSGEI 360
DB 301 LIIFANIPPEKVELFANKRKRTSSYEALEKGFIVCGNITVDSVTAFLRFLRDLKSGEI 360
QY 361 NTEIVFGEETPPSLELETIFKCYLAATTFISGSAMKEDLRRVAVESAECILIANPLCS 420
DB 361 NTEIVFGEETPPSLELETIFKCYLAATTFISGSAMKEDLRRVAVESAECILIANPLCS 420
QY 421 DSHADISNIMRVLSINRYDSTRIIIOLOSHNKVYLPRIPSNMMDGTGNIICFAELKL 480
DB 421 DSHADISNIMRVLSINRYDSTRIIIOLOSHNKVYLPRIPSNMMDGTGNIICFAELKL 480
QY 481 GFIDGGLVGLCTFELSLFVEONKRYMPKOTWKKHFLNSMKNILQRLSDDEAGSFP 540
DB 481 GFIDGGLVGLCTFELSLFVEONKRYMPKOTWKKHFLNSMKNILQRLSDDEAGSFP 540
QY 541 EVARLCEFLKMYLLDLAEYKSLFTDFGGLILNPPQVRIKNTLGFIAETPRDVRAL 600
DB 541 EVARLCEFLKMYLLDLAEYKSLFTDFGGLILNPPQVRIKNTLGFIAETPRDVRAL 600
QY 541 QVSRCLFVKLMLMIALIOHKPF - HSCCTILNPSQVRLNKDIFGFIADSSAAVRAE 599
DB 541 QVSRCLFVKLMLMIALIOHKPF - HSCCTILNPSQVRLNKDIFGFIADSSAAVRAE 599
QY 601 FYGCVCHDDVFIPELITNCGSKSRQHTIVPSYKRMKCLIGISSIISGODSPRRVAS 660
DB 601 FYGCVCHDDVFIPELITNCGSKSRQHTIVPSYKRMKCLIGISSIISGODSPRRVAS 660
QY 600 FYGCVCHDDVFIPELITNCGSKSRQHTIVPSYKRMKCLIGISSIISGODSPRRVAS 654
DB 600 FYGCVCHDDVFIPELITNCGSKSRQHTIVPSYKRMKCLIGISSIISGODSPRRVAS 654
QY 661 T-----SSISNFTRTLOHVEDODSDOLSSGMFMCPTSLDQVTKLRTGSK 709
DB 661 T-----SSISNFTRTLOHVEDODSDOLSSGMFMCPTSLDQVTKLRTGSK 709
QY 710 YKFNHIVACVFGDASHAPMGLRNFVPLRASNYTRKELDIYFISGLDYLOREMRFLRN 769
DB 710 YKFNHIVACVFGDASHAPMGLRNFVPLRASNYTRKELDIYFISGLDYLOREMRFLRN 769
QY 715 HEFQNHIVACVFGDASHAPMGLRNFVPLRASNYTRKELDIYFISGLDYLOREMRFLRN 774
DB 715 HEFQNHIVACVFGDASHAPMGLRNFVPLRASNYTRKELDIYFISGLDYLOREMRFLRN 774
QY 770 FPROIYLPAGALYSGDLHANIIEGSCMCAVLSPPROSSNOTVDTAIVATLIGSLQI 829
DB 770 FPROIYLPAGALYSGDLHANIIEGSCMCAVLSPPROSSNOTVDTAIVATLIGSLQI 829
QY 775 FPKHIMHIGSLYMGDLIAVNEBQSMCVILATYKALSSOILVDIAIMATLIGSLRI 834
DB 775 FPKHIMHIGSLYMGDLIAVNEBQSMCVILATYKALSSOILVDIAIMATLIGSLRI 834
QY 830 DSSSDPSVSEETPGYT - NGHNEKSNCRKVPILTELKNSNHFIEQLGLESLOETN 888
DB 830 DSSSDPSVSEETPGYT - NGHNEKSNCRKVPILTELKNSNHFIEQLGLESLOETN 888
QY 889 LHUSTAFSTGTVSSSFLDSLATAFYNYVLELQMLVYGVSSQLEOHLKDKYVGA 948
DB 889 LHUSTAFSTGTVSSSFLDSLATAFYNYVLELQMLVYGVSSQLEOHLKDKYVGA 948
QY 949 DSCSLSLGNRCKLGLSLHETILSDVNRNPFQGLFCSLDLFGILCYLVIIDEE 1008
DB 949 DSCSLSLGNRCKLGLSLHETILSDVNRNPFQGLFCSLDLFGILCYLVIIDEE 1008
QY 954 DQVEALISGRKRCGLGLSLDQVYVLSGINPRKTFGQLFCSLDLFGILCYLVIIDEE 1013
DB 954 DQVEALISGRKRCGLGLSLDQVYVLSGINPRKTFGQLFCSLDLFGILCYLVIIDEE 1013
QY 1009 LMPENKRFVITRPAEFKLLPSDLVFCALPFSTACYK 1045
DB 1009 LMPENKRFVITRPAEFKLLPSDLVFCALPFSTACYK 1045
QY 1014 PSQHRKRFVITRPAEFKLLPSDLVFCALPFSTACYK 1050
DB 1014 PSQHRKRFVITRPAEFKLLPSDLVFCALPFSTACYK 1050

OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RX MEDLINE=98026662; PubMed=9362339;
RA Morita T., Hanaoka K., Morales M.M., Montrose-Rafizadeh C.,
RA Guggino M.B.,
RT "Cloning and characterization of maxi K+ channel alpha-subunit in
RL rabbit kidney." 273:F615-F624(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RA Guggino M.B., Morita T., Hanaoka K., Wang S.-X.,
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF201702; AAF17562.1; -
DR InterPro: IPR000636; -
DR InterPro: IPR001622; -
DR InterPro: IPR002052; -
DR InterPro: IPR003006; -
DR InterPro: IPR003091; -
DR Pfam: PF00520; Ion_Trans; 1.
DR PRINTS: PR00169; KCHANNEL.
DR PROSITE: PS00290; IG_MHC; UNKNOWN.1.
DR PROSITE: PS00092; N6_MTASE; UNKNOWN.1.
SQ SEQUENCE 1171 AA; 131673 MW; A3CAA4E635215252 CRC64;

Query Match 41.28; Score 2359.5; DB 6; Length 1171;
Best Local Similarity 42.84; Pred. No. 1e-160;
Matches 495; Conservative 196; Mismatches 328; Indels 137; Gaps 21;

QY 26 AFLTSPVFEEGSLITLIFRLIMRSYK-KW-----QIKKGTIILEFTS 70
DB 26 AFLTSPVFEEGSLITLIFRLIMRSYK-KW-----QIKKGTIILEFTS 70
QY 71 GTI-----ARSHVRSILHFOGFRDHIEMLSAOTFVQVYLIVPLVLSIGSLIYFINS 124
DB 71 GTI-----ARSHVRSILHFOGFRDHIEMLSAOTFVQVYLIVPLVLSIGSLIYFINS 124
QY 75 GTLKPVEKEEAAVAEYGVMTSVDMAGVAMISQTLGRLVVLVPLSICALVIYRIDS 134
DB 75 GTLKPVEKEEAAVAEYGVMTSVDMAGVAMISQTLGRLVVLVPLSICALVIYRIDS 134
QY 125 ADYPGSSS-YEDKTIIDLVAFNAFFSYFGFLRFMAADKIKRWLENSIVDTIIPPTF 183
DB 125 ADYPGSSS-YEDKTIIDLVAFNAFFSYFGFLRFMAADKIKRWLENSIVDTIIPPTF 183
QY 135 SNLPESQNVKQFTLQIDMAFNVFLYFLGRLIANDKLELVNSVVDFTVPPVF 194
DB 135 SNLPESQNVKQFTLQIDMAFNVFLYFLGRLIANDKLELVNSVVDFTVPPVF 194
QY 184 ISYLYKSNMGLRFLRALRLLELPQIILRAIKTSNVSFKSLSTILSTWPTAAGFIH 243
DB 184 ISYLYKSNMGLRFLRALRLLELPQIILRAIKTSNVSFKSLSTILSTWPTAAGFIH 243
QY 195 VSYLYKSNMGLRFLRALRLLELPQIILRAIKTSNVSFKSLSTILSTWPTAAGFIH 254
DB 195 VSYLYKSNMGLRFLRALRLLELPQIILRAIKTSNVSFKSLSTILSTWPTAAGFIH 254
QY 244 LVNSGDPMLKGRNSQNSIYFESTIYLVWATTSTVFGDVAKTSLGRTFMEFLGS 303
DB 244 LVNSGDPMLKGRNSQNSIYFESTIYLVWATTSTVFGDVAKTSLGRTFMEFLGS 303
QY 255 LVNSGDPMLKGRNSQNSIYFESTIYLVWATTSTVFGDVAKTSLGRTFMEFLGS 314
DB 255 LVNSGDPMLKGRNSQNSIYFESTIYLVWATTSTVFGDVAKTSLGRTFMEFLGS 314
QY 304 FANIPPEKVELFANKRKRTSSYEALEKGFIVCGNITVDSVTAFLRFLRDLKSGEI 363
DB 304 FANIPPEKVELFANKRKRTSSYEALEKGFIVCGNITVDSVTAFLRFLRDLKSGEI 363
QY 315 FASVPEELIELIGRKKYGGSYSAVSGRKHIVCGHITLLESVSNFLDKORDVDVE 374
DB 315 FASVPEELIELIGRKKYGGSYSAVSGRKHIVCGHITLLESVSNFLDKORDVDVE 374
QY 364 IVFGEETPPSLELETIFKCYLAATTFISGSAMKEDLRRVAVESAECILIANPLCS 423
DB 364 IVFGEETPPSLELETIFKCYLAATTFISGSAMKEDLRRVAVESAECILIANPLCS 423
QY 375 IVFGEETPPSLELETIFKCYLAATTFISGSAMKEDLRRVAVESAECILIANPLCS 434
DB 375 IVFGEETPPSLELETIFKCYLAATTFISGSAMKEDLRRVAVESAECILIANPLCS 434
QY 424 AEDISNIMRVLSINRYDSTRIIIOLOSHNKVYLPRIPSNMMDGTGNIICFAELKL 483
DB 424 AEDISNIMRVLSINRYDSTRIIIOLOSHNKVYLPRIPSNMMDGTGNIICFAELKL 483
QY 435 AEDASNIMRVLSINRYDSTRIIIOLOSHNKVYLPRIPSNMMDGTGNIICFAELKL 494
DB 435 AEDASNIMRVLSINRYDSTRIIIOLOSHNKVYLPRIPSNMMDGTGNIICFAELKL 494
QY 484 AOCGLVPGCLTFELSLFVEONKRYMPKOTWKKHFLNSMKNILQRLSDDEAGSFP 543
DB 484 AOCGLVPGCLTFELSLFVEONKRYMPKOTWKKHFLNSMKNILQRLSDDEAGSFP 543
QY 495 AOCGLVPGCLTFELSLFVEONKRYMPKOTWKKHFLNSMKNILQRLSDDEAGSFP 554
DB 495 AOCGLVPGCLTFELSLFVEONKRYMPKOTWKKHFLNSMKNILQRLSDDEAGSFP 554
QY 544 RLCEFLKMYLLDLAEYKSLFTDFGGLILNPPQVRIKNTLGFIAETPRDVRAL 603
DB 544 RLCEFLKMYLLDLAEYKSLFTDFGGLILNPPQVRIKNTLGFIAETPRDVRAL 603
QY 555 ELCEFLKMYLLDLAEYKSLFTDFGGLILNPPQVRIKNTLGFIAETPRDVRAL 612
DB 555 ELCEFLKMYLLDLAEYKSLFTDFGGLILNPPQVRIKNTLGFIAETPRDVRAL 612

Prfam; PF00520; Ion_trans; 1.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
DR PROSITE: PS00092; N6_MTASE; UNKNOWN_1.
KW Ionic channel.
SEQUENCE 1151 AA; 128933 MW; 24E62FE0C1D94015 CRC64;

Query Match 41.2%; Score 2357.5; DB 6; Length 1151;
Best Local Similarity 43.2%; Pred. No. 1.4e-160;
Matches 488; Conservative 194; Mismatches 341; Indels 107; Gaps 18;

QY 15 PKMSC-----TTEIOA-----AFLLSFVTFPFGSLIILIRLIRSVK-KW----- 55
DB 37 PKMDALIIPVMEVPCDSRGORMMNAFLASSVTFEGGLFI---LIMRLIKYLMTVCC 92
QY 56 -----OIKGTGIIILEFTSGTI-----ARSHVRSIHFQGFORDHIELLSAQT 99
DB 93 HCGGKTKAOKIKNGSS-----QADGTILKPYDEKEEAVAAGWMTSVKMDAGVMSIQT 147
QY 100 FVGQVILVLFVLSIGSLIIFINSADPVGSSS--YEDKTIPIDLVFNAFFSFGFLRFM 158
DB 148 LTGRVLVYLVFALSIGALVIYFIDSNPESQNFYKQFTQIDMAFNVFLLYGLAFI 207
QY 159 AADKIKFWLENSIVDFTIPPTISYLYKSNWLGRLRLRLLELPQIILIRAIKT 218
DB 208 AANDKLMFMLEVNSVYDFEYVPPVSVYLNRSWGLRFLRLRIQFSEILOFLNLT 267
QY 219 SNSVFSKLLSTIISTWFTAGFIHLVENSQDPMUKGRNSQISYFESYLYVMATTSYVG 278
DB 268 SNSIKLVNLSIFISTWTLTAAGFIHLVENSQDPMENFQNNALTYWECVYLLMTVMSYVG 327
QY 279 FGDVVAKTSLGRTFIMFTLGLSLIFANYPIMVELFANKRKYTSYSEALGKKFTIYVG 338
DB 328 YGDYAKTTLGLRFLVFFLIGLMAFASYVPEIILIGNRKYGGSYGASRKRIIVCG 387
QY 339 NITVDSVAFNLNLRDSEGLINTEIVELEGETPSLEDETIFFKCYLAATYFISGAMKE 398
DB 388 HTLESVGNFLKDFLHKRDQVNEIVEFLHNSPMLLEALFKRHFTQVEYFGQSVLNP 447
QY 399 DLRAVVASAECLIANAPLCSDAEDISNMRVLSKNDSTRIITQIILQSNKYLL 458
DB 448 DLARKIESADACILANKYCADPDAEDASNIMRYISIKNHPKIRITOMQYNNKHL 507
QY 459 PRIPSMNDGTGNICFPAELKLGFIAGGLVGLCTPLTSLFVEQNKVMPQOTKKHFL 518
DB 508 LNPISNMKKEGDAICLAEIKLIGFTAGSLAGSLTMLANLFMSAFIKIEDTQKYLL 567
QY 519 NSMKKILITQLRSLDFAGMSPEVARLCEFLKYYLLLIAIEYKSLFTDFGCGIILNPQV 578
DB 568 EGVSNEMYTEYLSSAFVGLSPFTVCELCFVKLKLMAIEYKSANRES--RILINPQNL 625
QY 579 RIRKNTLGFIAETPKDVRALFYCSVCHDVFIPELITNCCGKRSRNOHITVPSVKRK 638
DB 626 KIQETELFFIASDAKEVRAFFYKACHDITDPKRIKKCCGCK--RIEDBQPTLSLPK 682
QY 639 KCLKISIRISIGQDAP-----PRVASTSISINFTTRTLQDVVDQSDQLDSCGMFHC 692
DB 663 KKGRRGGRNNSNSPKLMRHPLLIPGNDQIDN-----MDSNKKYDSTGMFHC 733
QY 693 KFTSLDKVTLKRTGSKYKFRNHIVACYFGDAHSAFPMGLRNFVMDLRASNYTRKELDIV 752
DB 734 APKEIEKYLITRSEAAAFVLSGHVYVVCIFGDVSSALIGLRNLYMPLRASNFIYHELKHLV 793
QY 753 FGLSDYLOREKRLRNPQIYILPGCALYSGLDAAANEQSCMAVLSPRPQSPNQTL 812
DB 794 FVGSLEYLKRREKRETLNHPKVSILPGLPLSRADLRANVINCDDKCVILSANONNIDVSL 853
QY 813 VDETAIMATLTIGSLQID-----SSDPSPSVSE--ETPGYTGCHN 851
DB 854 QDKKEILASLNKSMQFDSIGVLANSGGFTPPGMDRSSPNSVYHGLRLRPSTTTGCVN 913
QY 854 EKSNCRKVPILTLELNPSNIHIEQLGLEGSLQETNLHLSTAFSTGTVFSSFLDLSLA 911

DB 914 -----IPITTELVDNTNVQFLD---DDDDPDPTELYLTQPFACGTAFVAVSLDLSMS 963
QY 912 TAFVYHVELLQMWYGVGSSOLEQHLDKDKYGVADSCSTLSLGRNCKLGLSLHET 971
DB 964 ATYENDNITLIRLTVTGATPELEALIAENALRGYSTPOTLANRRCRAQALALDGG 1023
QY 972 ILSDVNPRNTFGQLFCGSLDFGLICVGLYRIDEEELNPE--NKRFTYTPRANFKLLP 1029
DB 1024 PEADGDGGCGYDGLCKALKTKYNNMCFGIYLRDAHLSTPSCGTRRYVITNPPYEFELVP 1083
QY 1030 SDLVCAIPFSTACKRNEEFSLQKSYEIVNKAQSTTDTDRHKLISSPL 1079
DB 1084 TDLIFCLMQF-----DHNAGOSRASLSHSHSSOSSSKSSSVSHSI 1124

RESULT 6
ID Q12921 PRELIMINARY; PRT; 1154 AA.
AC Q12921;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE CALCIUM ACTIVATED POTASSIUM CHANNEL.
GN HSLQ.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=95085775; PubMed=7993625;
RX Tseng-Crank J., Foster C., Mertz R., Godinot N., Reinhart P.;
RT "Cloning, expression, and distribution of functionally distinct
Ca(2+)-activated K+ channel isoforms from human brain.";
RL Neuron 13:1315-1330(1996).
DR EMBL; U11717; AAC50353.1; -.
DR InterPro; IPR000636; -.
DR InterPro; IPR001622; -.
DR InterPro; IPR002052; -.
DR InterPro; IPR003006; -.
DR Pfam; PF00520; Ion_trans; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR PROSITE; PS00092; N6_MTASE; UNKNOWN_1.
KW Ionic channel.
SEQUENCE 1154 AA; 129231 MW; 22C4DB64BC251D51 CRC64;

Query Match 41.2%; Score 2356.5; DB 4; Length 1154;
Best Local Similarity 43.2%; Pred. No. 1.7e-160;
Matches 488; Conservative 193; Mismatches 342; Indels 107; Gaps 18;

QY 15 PKMSC-----TTEIOA-----AFLLSFVTFPFGSLIILIRLIRSVK-KW----- 55
DB 40 PKMDALIIPVMEVPCDSRGORMMNAFLASSVTFEGGLFI---LIMRLIKYLMTVCC 95
QY 56 -----OIKGTGIIILEFTSGTI-----ARSHVRSIHFQGFORDHIELLSAQT 99
DB 96 HCGGKTKAOKIKNGSS-----QADGTILKPYDEKEEAVAAGWMTSVKMDAGVMSIQT 150
QY 100 FVGQVILVLFVLSIGSLIIFINSADPVGSSS--YEDKTIPIDLVFNAFFSFGFLRFM 158
DB 151 LTGRVLVYLVFALSIGALVIYFIDSNPESQNFYKQFTQIDMAFNVFLLYGLAFI 210
QY 159 AADKIKFWLENSIVDFTIPPTISYLYKSNWLGRLRLRLLELPQIILIRAIKT 218
DB 211 AANDKLMFMLEVNSVYDFEYVPPVSVYLNRSWGLRFLRLRIQFSEILOFLNLT 270
QY 219 SNSVFSKLLSTIISTWFTAGFIHLVENSQDPMUKGRNSQISYFESYLYVMATTSYVG 278
DB 271 SNSIKLVNLSIFISTWTLTAAGFIHLVENSQDPMENFQNNALTYWECVYLLMTVMSYVG 330
QY 279 FGDVVAKTSLGRTFIMFTLGLSLIFANYPIMVELFANKRKYTSYSEALGKKFTIYVG 338

Db 331 YGVYATTTGRLFMVFFILGGLAMFASVYPEITELLIGNRKKKGGSSAVSGRHHVVC 390
339 NITVDVTAFLRNLFRDKSGEINTEIVFLGETPSPLEETIFKCYLAATTFFISSAMKE 398
391 HITLESYVNFLLKDFLHKDRDVNVEIVFLNHSINPLELEALFKRHFPQVEVYGSVLPNH 450
399 DLRAVAESAACILIANPLCSDSHADISINIMVLSIKYNDSTTRIIIOLOSCHKVYL 458
451 DLARVKIESADACILIANKKCADPADASINIMVLSIKYHPKIRITOTMLQYHNKAHL 510
459 PKIRSMMDGDNIICFAELKGLFIAOGCLVPGCTFTSLFVBNKVMKPKWKKHFL 518
511 LNIPSNMKEGDDAICLAELKGLFIAOSCLAOGSLTMLANFMSRSTIKLEEDWOKYTL 570
519 NSMKNKILTORLSDDFAGMSPEVVARLCFLKMYLLLAIEYKSLFTDGFGLILNPPPOV 578
571 EGVSENEYTEVTLSSAFVGLSPYVCELCFVKLKLMIAIEYKSNRBS--RIILNPGNHL 628
579 RIRKNTIGFFIAETPKVRRALFYCSVCHDDVFIPELITNCGCKSRKROHTVPSVKRM 638
629 KIOGTLGFFIASDAKEVKRAFECACHDITDPKRIKCGCK--RLDEQOSTLSPK 685
639 KCLGISSRISGODSP-----PRVSASTSSISNFTTRLOHVEDOPSDDOLSSGMFHW 692
686 KKGNGGMRNSPNTSPKLMRHPDPLIFGNDQIDMDSHVKKY-----DSTGMFHW 736
693 KPTSLDVTLLKRTGSKYKFRNHIVACVFGDASAPGLRNFVPLRASNYTRKELDIY 752
737 APRIEKVIILTRSEAAMTVLSGHVYVCIFGDVSALIGLRNLVPLRASNFHYHELKHIV 796
753 FVIGSLDLOVRMRFLRNPPOYIILPGCALYSGDLHAANIEGSCMCVLSPPPOSSQTL 812
797 FVSGIEYLRKREMETLANPKVSLPGTPLSRADLRVAINICDVCYLISANONNIDTSL 856
813 VDFEAINATLITIGSLQID-----SSSDPSPVSE--ETPGYTNCHN 851
857 QDKKCIASLNKIKMOPDDISGLVQANSQGTTPRGMDRSSPDNSPVHGLMRQPIITTCVN 916
852 EKSKCRKVPILTELKNSNHFIFOLGLEGSLQETLNLHLSSTAGTGVSSFLDSILA 911
917 -----IPITTELVDNTNOFLODQ---DDDDDDPTTELITOPACGTAFVSVLDSIMS 966
912 TAFVNVHVELLOMLVTVGVSOSLEOHLDKQVYGVADSCSLSSGNRCGLSLSHET 971
967 ATYVNDILITRLTVGGATPELEALIAEENALRGYSTPOTLANDRCVAVOALALDG 1026
972 ILSDVNRNFTFGQLFCGSLDFGILCVGLYRIIDEELNPE--NKRPVITPRAEFKLLP 1029
1027 PFALDGGGGCGDLFCALAKTYNMLFCGYIRLRAHLSSTPQCTKRYVITNPRYEFELVP 1086
QY 1030 SDLVFCAIPSTACVYKRNNEFSLOKSEIYVKNASQTTEDTFRHKLSSHPL 1079
Db 1087 TDLIFCLMOF-----DHNAGOSRASLSHSSSSSSSSKSSVHSI 1127

RESULT 7
Q9UBB0 PRELIMINARY; PRT: 1154 AA.
AC Q9UBB0; 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE CALCIUM-ACTIVATED POTASSIUM CHANNEL ALPHA SUBUNIT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LENS EPITHELIUM;
RA Rae J.L., Shepard A.R.;
RT "Identification of potassium channels in human lens epithelium.";
RL (in) Civan M.M. (eds.);

RL Current topics in membranes. The eye's aqueous humor - from secretion
RL to glaucoma, pp.45:69-104, Academic Press, San Diego (1998).
DR EMBL: AF025999; AAB88802.1; -
DR InterPro: IPR000636; -
DR InterPro: IPR001623; -
DR InterPro: IPR002052; -
DR InterPro: IPR003066; -
DR InterPro: IPR003091; -
DR Pfam: PF00520; Ion_trans. 1.
DR PRINTS: PR00169; CHANNEL.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
DR PROSITE: PS00092; N6_MTASE; UNKNOWN_1.
KW Ionic channel.
SQ SEQUENCE 1154 AA; 129208 MM; 621F18A4DE7BD274 CRC64;

Query Match 41.2%; Score 2356.5; DB 4; Length 1154;
Best Local Similarity 42.9%; Pred. No. 1.7e-160;
Matches 487; Conservative 197; Mismatches 333; Indels 119; Gaps 19;

QY 15 PKMSC-----TTEIOA-----AFILSFVTFEFGILYILFLIRLSVK-KW---55
Db 40 PKMDALLIPTMEVPCDSRGQRMMAFLASSMYTFEGGLFII---LMTKTKLMTVCC 95
QY 56 -----QIKGTGIIILEFTSGT-----ARSHVSLHEOGQFRHIEMLSAQT 99
Db 96 HCGGKTEAQRKINNSS-----QADGTLKPYDEKEEVAEVEGMMTYSKWAGYMISAQT 150
QY 100 FVGQVILVFLVSLIGSLIIFYINSADPVGCS--YEADKTIPTDVLVNAFSEFGFLRFM 158
Db 151 LTGKVLVVLVFLALSTGLVLYIFIDSSNPISCONFYDFLOIDMAPNVFLYFGRLFI 210
QY 159 AADKIKFMLEMNSYDIETIPTFTISYLYKSNMGLRFLRALRLLEPILOILRAKT 218
Db 211 AANDKLFMLEVANSYVDFTVPVYFVSVYLNRSWLGRLFLRALRLLOFSEILOFLNLT 270
QY 219 SNSVKEKLSLITLSTFTAGFTAGFTIYVNSGDPLKRNONSIPESITLVMAATSTVG 278
Db 271 SNSIKLVNLSTFTSTVLTAAGFTIHLVNSGDPEPNFONNOLVYWCYVLLVMTVSTG 330
QY 279 FGDVAVTSGLRTEIMFTTGLSLILFANYIPEWELEFANKRYTSYEALAKKFTVVC 338
Db 331 YGVYATTTGRLFMVFFILGGLAMFASVYPEITELLIGNRKKKGGSSAVSGRHHVVC 390
QY 339 NITVDVTAFLRNLFRDKSGEINTEIVFLGETPSPLEETIFKCYLAATTFFISSAMKE 398
Db 391 HITLESYVNFLLKDFLHKDRDVNVEIVFLNHSINPLELEALFKRHFPQVEVYGSVLPNH 450
QY 399 DLRAVAESAACILIANPLCSDSHADISINIMVLSIKYNDSTTRIIIOLOSCHKVYL 458
Db 451 DLARVKIESADACILIANKKCADPADASINIMVLSIKYHPKIRITOTMLQYHNKAHL 510
QY 459 PKIRSMMDGDNIICFAELKGLFIAOGCLVPGCTFTSLFVBNKVMKPKWKKHFL 518
Db 511 LNIPSNMKEGDDAICLAELKGLFIAOSCLAOGSLTMLANFMSRSTIKLEEDWOKYTL 570
QY 519 NSMKNKILTORLSDDFAGMSPEVVARLCFLKMYLLLAIEYKSLFTDGFGLILNPPPOV 578
Db 571 EGVSENEYTEVTLSSAFVGLSPYVCELCFVKLKLMIAIEYKSNRBS--RIILNPGNHL 628
QY 579 RIRKNTIGFFIAETPKVRRALFYCSVCHDDVFIPELITNCGCKSRKROHTVPSVKRM 638
Db 629 KIOGTLGFFIASDAKEVKRAFECACHDITDPKRIKCGCK--RLDEQOSTLSPK 685
QY 639 KCLGISSRISGODSP-----PRVSASTSSISNFTTRLOHVEDOPSDDOLSSGMFHW 692
Db 686 KKGNGGMRNSP-----NTSPKLMRHPDPLIFGNDQIDMDSHVKKTDST 730
QY 687 GPFHMKPTSLDKVTLKRTGSKYKFRNHIVACVFGDASAPGLRNFVPLRASNYTRK 746
Db 731 GPFHMKAPKEIEKVIILTRSEAAMTVLSGHVYVCIFGDVSALIGLRNLVPLRASNFHYH 790
QY 747 ELKDIVTIGSLDYLQREMRFLRNPPOYIILPGCALYSGDLHAANIEGSCMCVLSPPPO 806

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Db 791 ELKHIVFGSIEYLKREMBETLHNPFXKSLPGLSRADLRVNTNLCDMCVILSANQNN 850
Oy 807 SSNOGLVTEALMATLTGSLQID-----SSDPSPSVSE-ETPG 845
Db 851 IDDTSLQDKECLASLNKSMQFDDISIGVLQANSQGFPPGMDRSSPNSPVHGMRLRPS 910
Oy 846 YTNCHNEKSNCRKVPILTELKNPSNIHFIHQGLGSLQETNHLNLSAFSGTAFSSSF 905
Db 911 ITTGVN-----IPITELVNDVNWQFLDQ---DDDDDPTELTLTPGFACGTAFAVS 960
Oy 906 LDSLATAFYNYHYVLELQMLVTGVSQSLQEHLDKRVYGVADSCSTLSGRNCKLGL 965
Db 961 LDSLSATYFPNDILTLRLTYTGATPELEALINEENALNGYSTPQTIANRDCRVAQ 1020
Oy 966 LSLHETILSDVNPRTFQGLFCGSLDLFGILCVGLYRIIDEELNPE--NKRFTVTRPAN 1023
Db 1021 LALDGPADLDGCGCYDLCFKALKTYNMLCFGIYRLRDAHLSTPSCOTKRYVITNPPY 1080
Oy 1024 EFKLPSDLVFCALPFSNACYKRNNEFSLOKSYELVNKASQTEDETFPHKLSHPL 1079
Db 1081 ERELVPDILFLCMQF-----DHNAQGRASLSHSHSSOSSSKSSSVHSI 1127

RESULT 8
O12960 PRELIMINARY: PRT: 1178 AA.
AC O12960
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE LANGE-CONDUCTANCE CALCIUM-ACTIVATED POTASSIUM CHANNEL.
GN HSGO.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-SUBSTANTIA NIGRA BRAIN TISSUE;
RX MEDLINE=95182815; PubMed=7877450;
RA Dorelitzky S.I., Trojnecki J.T., Gribkoff V.K.;
RT "Cloning and expression of a human large-conductance calcium-activated
RT potassium channel."
RL Brain Res. Mol. Brain Res. 27:189-193(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-SUBSTANTIA NIGRA BRAIN TISSUE;
RX MEDLINE=93318148; PubMed=7687074;
RA Butler A., Tsunoda S., McCobb D.P., Wei A., Salikoff L.;
RT "mslo, a complex mouse gene encoding 'maxi' calcium-activated
RT potassium channels."
RL Science 261:221-224(1993).
DR EMBL: U13913; AA85104.1; -.
DR InterPro: IPR000636; -.
DR InterPro: IPR001622; -.
DR InterPro: IPR002052; -.
DR InterPro: IPR003006; -.
DR Pfam: PF00520; Ion_Ctrans; 1.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
DR PROSITE: PS00092; N6_MTASE; UNKNOWN_1.
KW Ionic channel.
SO SEQUENCE 1178 AA; 131026 MW; 4F00800A725948B2 CRC64;

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Query Match 41.2%; Score 2356.5; DB 4; Length 1178;
Best Local Similarity 42.9%; Pred. No. 1.7e-160;
Matches 487; Conservative 197; Mismatches 333; Indels 119; Gaps 19;

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Oy 15 PKMSC-----TTEIDA-----AFITSSVTFPSGILILLIRLLMRSK-KW----- 55
Db 64 PKMDALITPVTMEVPCDSRGQRMMWAFIASSKVTFFGGLEIF---LIMRLKLYIMTVCC 119

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Oy 56 -----QIKGTGILLETSGTI-----ARSHVRSIHFGQGRDHIEMLSAQT 99
Db 120 HCGGKTRKAQKINNGSS-----QADGTLKPYDEKEEAALAEAGWTSVKDNAGVWISAQ 174
Oy 100 FVGQVLVLEVLVSLISGLIIVEINSADVPSCSS-YEDKTIPIDLVFNAPFSFGFLRFM 158
Db 175 LTGRVLVLEVLVSLISGLIIVEINSADVPSCSS-YEDKTIPIDLVFNAPFSFGFLRFM 158
Oy 159 AADKIKVLEWENSLVDFITPTPTISYLYKSNMGLRFLRALRLLELPQLQILRAIKT 218
Db 235 AANDKMFMLEVNSVVDFTVPVFSVYLNRSWGLFLRALRLIQSEILQFINILKT 294
Oy 219 SNSVFSKLSLITSTWTAAGFIHLVENSQDPMKGNNSONISFESEIYVMAATTSVG 278
Db 235 SNSIKLVNLSIFSTWLAAGFIHLVENSQDPMKGNNSONISFESEIYVMAATTSVG 278
Oy 279 FGDVVAKTSIGRTFIMPTLSGLIFANVYIPENVELFANKRKYSSYBALGKKFTVCG 338
Db 355 YGDVVAKTTLGRFVVFITLGLAMFASYPEIIEILGNRRKYGSGYSVAGRKHIYVCG 414
Oy 339 NITDVSATFLRNLRLDKSGEINTEIYVFLGETPPSLEETIFKCYLATYTTISGAMKE 398
Db 415 HITLESVSNFLKDFLAKRDVDVNEIYVFLHNIISPLLEALFKRHFTQVEFYQSVLNP 474
Oy 399 DLRRVAVSEACLTIANPLCSDSHAEIDISNIMRYLSIKNDSTRTITILQSHNKVYL 458
Db 475 DLARKIESADCLILAKYKCADPDADASINIRYISIKNHPIKRIITOMLOTHNKVNL 534
Oy 459 PKIPSMNDQDNILCFPAELKLGFLAQCLVPLGCTPLTSLFEVEONKVMKPTKKHFL 518
Db 535 LNIPSMNKEGDALCLAEKLGFLAQCLVPLGCTPLTSLFEVEONKVMKPTKKHFL 518
Oy 519 NSMKKILTORLSDDFACMSPEVARLCLFKMYLLILIEKSLFTDQFCGLILNPPQV 578
Db 595 EGVSNEMYTEYLSAFVGLSEPTVCELCFVKLKLMIIEKSNARES--RILNPNHNL 652
Oy 579 RIRKNTLGFIAEPKDVRLFLFYCVCHDDVPELITNCGCKSRSONHTVPSVKRM 638
Db 653 KIQGETLGFIAEPAKAEKRAFFYCKACHDITDPKRIKKCGCK--RLDEQPSYLSPK 709
Oy 639 KCLKGISRISIGQDPPPVASSTSSISNFTRTLOHD-----VEQDSQDQLDS 686
Db 710 K-----KQRNGGMKNSP-----NTSPILMRHDLPLPGNDQIDNMSNVKKYST 754
Oy 687 GMFWCKPTSLDKVYLAKTKGSKYKFRNHVYACVFGDAHSAPMGLRNVMPLRASNYTRK 746
Db 755 GMFWCKAPEKEIKVILTRSELAAMTVLSGHVYVCIFGVDSALIGLRNLMPLRASNFHYH 814
Oy 747 ELKQIVFGSLDYLOREKRFNRNPOIYILPGCALYSGDLAANAEGCSMKCAVLSPPQP 806
Db 815 ELKHIVFGSIEYLKREMBETLHNPFXKSLPGLSRADLRVNTNLCDMCVILSANQNN 874
Oy 807 SSNOGLVTEALMATLTGSLQID-----SSDPSPSVSE-ETPG 845
Db 875 IDDTSLQDKECLASLNKSMQFDDISIGVLQANSQGFPPGMDRSSPNSPVHGMRLRPS 934
Oy 846 YTNCHNEKSNCRKVPILTELKNPSNIHFIHQGLGSLQETNHLNLSAFSGTAFSSSF 905
Db 935 ITTGVN-----IPITELVNDVNWQFLDQ---DDDDDPTELTLTPGFACGTAFAVS 984
Oy 906 LDSLATAFYNYHYVLELQMLVTGVSQSLQEHLDKRVYGVADSCSTLSGRNCKLGL 965
Db 961 LDSLSATYFPNDILTLRLTYTGATPELEALINEENALNGYSTPQTIANRDCRVAQ 1044
Oy 966 LSLHETILSDVNPRTFQGLFCGSLDLFGILCVGLYRIIDEELNPE--NKRFTVTRPAN 1023
Db 1045 LALDGPADLDGCGCYDLCFKALKTYNMLCFGIYRLRDAHLSTPSCOTKRYVITNPPY 1104
Oy 1024 EFKLPSDLVFCALPFSNACYKRNNEFSLOKSYELVNKASQTEDETFPHKLSHPL 1079
Db 1105 ERELVPDILFLCMQF-----DHNAQGRASLSHSHSSOSSSKSSSVHSI 1151

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RESULT 9
013150 PRELIMINARY; PRT: 1178 AA.
AC 013150;
AC 013150;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE CALCIUM-ACTIVATED POTASSIUM CHANNEL.
GN HSL0.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=ACORTIC SMOOTH MUSCLE, AND UMBILICAL SMOOTH MUSCLE;
RX MEDLINE=96024676; PubMed=7573516;
RA McCobb D.P., Fowler N.L., Featherstone T., Lingle C.J., Salto M.,
RA Krause J.E., Salkoff L.;
RT "A human calcium-activated potassium channel gene expressed in
RT vascular smooth muscle."
RL Am. J. Physiol. 269:H767-H777(1995).
DR EMBL: U23767; AAA92290.1; -.
DR InterPro: IPR000636; -.
DR InterPro: IPR001622; -.
DR InterPro: IPR002052; -.
DR InterPro: IPR003006; -.
DR Pfam: PF00520; Ion_trans; 1.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
DR PROSITE: PS00092; N6_MTASE; UNKNOWN_1.
KW Ionic channel.
SQ SEQUENCE 1178 AA; 130998 MW; AD3C9634F8A21EEC CRC64;

Query Match 41.2%; Score 2356.5; DB 4; Length 1178;
Best Local Similarity 42.9%; Pred. No. 17e-160;
Matches 487; Conservative 197; Mismatches 333; Indels 119; Gaps 19;

QY 15 PKMSC-----TTEIOA-----AFLSSVTFSSGLILILIRLIRSVK-KW-----55
DB 64 PKMDALIPVMEVPCDSRGORMMMAFIASSMTVFEGGLFI-----LLMPTKYLMTVCC 119

QY 56 -----QIKGTGILLETSGT-----ARSHVRLHOGQGRDIEMLISQOT 99
DB 120 HCGGKTEAOKINNGS-----QADGTLKPYDEKEEAFAAEVGMTSYKADGAWISQOT 174

QY 100 FVGQVLIVLVLSIGSLIIFYINSADPVGSCSS-YEDKTPIDLVFNAPFSFGLEFEM 158
DB 175 LTGVLVIVLVFALSIGALVIFYIDSSNPDESCQNFYDFTIQIDMAFVVFLLYFGLRFI 234

QY 159 AADKIKFWLEMSIVDIETPTPTFISYLYKSNMGLFLRALRLLELPQIILIRAIKT 218
DB 235 AANKLFWLEWNSVVDFFVPPVFSVYLLNRSWLGLEFLRALRLIOPSEILQIFNLTKT 294

QY 219 SNSYKFSLLIISTFTAGFTHLVENSGDPLKGNISNISEYIEIYVMAITSYG 278
DB 295 SNSIKLVNLSIFSTYLTAGFTHLVENSGDPWENFQNNQALTYWECVYLLMTVSTVG 354

QY 279 FGDVVAATSLGRTEFTFTGLSLILFANYIPENWELFANKKRYSSYEALKGKRFIVCG 338
DB 355 YGDVVAATTLGRLEFVFIIGLMAFSYVEIIEILGNKRKYGGSASVGRKHIVYCG 414

QY 339 NITVDSYATLRLNRLRDKSGEINTEIYFLGTTPPSLEETIFKCYLAVTTPISGSANKWE 398
DB 415 HITLESYVNFLEKDLKRDORDVNEIYFLHNISPNLELEALFKRHFPQVEYQGSVLNPH 474

QY 399 DLRAVAVESAACILIANPLCSDSHADISIMAVLSKANDSTRTIITQLQSHNKVYL 458
DB 475 DLAVKTESADACILINKKACADDAEDASNIMRVISIKNPKRIRITOMLQYHNKRAHL 534

QY 459 PKISMMMDTGDNITICAFELKGLFIAOGCLVPGCTFTLSFLVSONKVMKQMKKHFEL 518
DB 535 LNTFSNMKREDDAICLAELKGLFIAOGCLVPGCTFTLSFLVSONKVMKQMKKHFEL 594

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QY 519 NSMKKILTORLSDDFAGMSPEVARLCFLMYLLIAIEYKSLFTDGFCLILNPPQV 578
DB 595 EGVSNEMYETELSSAFVGLSEPTVCELCFVKILMLIAIEYKSANRES--RLINPGNHL 652

QY 579 RIRKNTLGFIAEPKQVRRALFCSYCHDVFIPELITNCGCKSRSGHITVSYKMK 638
DB 653 KIOEGTLEFFIASPAKKEKRAFFCKACHDITDPKRIKCGCK--RLEDEQSTLSPK 709

QY 639 KCLGISIRISGODSPPVASSTSSISNFTTRLOHD-----VEQDDQLDSS 686
DB 710 K-----KRNKGMRNSP-----NTSPKLRHDPDLLPGDQIDNMSNVRKIDST 754

QY 687 GMFHCKPTSLDKVTLKRTGSKYFRNHIVACYFGDAHSPMGIRNFMPLRASNTTRK 746
DB 755 GMFHCAKPEIKETKYLRTSEAAAMVLSGHVVCIFGDVSSALIGRLNMLPRLASNFHYH 814

QY 747 ELKDIVFSGIDYLOREHRLFRNPQIYILGCLALSSDILAANIEQCSMCVAVSPRPQ 806
DB 815 ELKHIVFSGISTEYLRKRETHLHNEPKVSIPLPTPLSRADLRAVINILCDMVCILANONN 874

QY 807 SSNOTLVDTAIMATLTIGSLQID-----SSDPSPSVSE-ETPG 845
DB 875 IDDTSLQDKECILASLNKSMQFDDSGIVLOANSOGFTPPGMDSSPDNSPVHGMILQPS 934

QY 846 YTNHNEKSNCRKVPILTCLNPSNIHETIQLGLESGLQETNHLSTAFSTGVFSSSF 905
DB 935 ITTGVN-----IPITELVNDTNVOFLDQ-----DDDDDPTELYLQPFACATFAVSV 984

QY 906 LDSLATLAFYVHYVHLELLOMLVYTGVSQSLQEHLDKDKVYVAASCSLISGRNRCKGL 965
DB 985 LDSLMSATVFENDNLTILRLVLTGTGATPELEALAEENALRGYSTPOTLANRRCRAVQ 1044

QY 966 LSLHETILSDVNPRTNFGQLFCGSLDLFGILCYGLYRIIDEELNPE--NKRFTYTRPAN 1023
DB 1045 LALLDGPADLDGCGCYDGLFCRKLKTYNMLCFGILRLADHLSTPSCQTRYIYITNPPY 1104

QY 1024 EFKLLPSDLVECAIPFSTACYKRNEEFSLOKSYEIVNKASQTTEDTRHKLSSHPL 1079
DB 1105 EFELVPTDLICLQMVF-----DHNAGOSRASLSHSSSSSKSSSVSHSI 1151

RESULT 10
Q12917 PRELIMINARY; PRT: 1113 AA.
AC Q12917;
AC Q12917;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
DE CALCIUM DEPENDENT POTASSIUM CHANNEL ALPHA SUBUNIT.
GN MAXIK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=MYOMETRIUM;
RX MEDLINE=96196569; PubMed=8612769;
RA Meera P., Wallner M., Jiang Z., Toro L.;
RT "A calcium switch for the functional coupling between alpha (hsl0) and
RT beta subunits (kv.ca beta) of maxi K channels.";
RL FEBS Lett. 382:84-88(1996).
DR EMBL: U11058; AAB65837.1; -.
DR InterPro: IPR000636; -.
DR InterPro: IPR001622; -.
DR InterPro: IPR002052; -.
DR InterPro: IPR003006; -.
DR Pfam: PF00520; Ion_trans; 1.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
DR PROSITE: PS00092; N6_MTASE; UNKNOWN_1.
KW Ionic channel.
SQ SEQUENCE 1113 AA; 125210 MW; 1D9A857F69106CE8 CRC64;

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Query Match 41.2%; Score 2355.5; DB 4; Length 1113;
 Best Local Similarity 43.4%; Pred. No. 1.9e-160;
 Matches 482; Conservative 196; Mismatches 328; Indels 105; Gaps 17;

QY 26 AFILSSVFTEFSGILILILIFRLIRSVK-KW-----QIIKGTGIIILEFTS 70
 DB 24 AFLASSVTFEFGGLFI-----LMRLTKYLMVTVCCHCGGKTEAKKINNGSS-----QAD 74

QY 71 GTI-----ARSHVRSJLHFOGQFRDHIEMLSAQTVEGQVLYLVFVLSIGSLIYFINS 124
 DB 75 GTLKPVDKEEAAVAEYGMWTSVKDMAGVMISAOTLTGRVLVYLVFALSIGALVIYFIDS 134

QY 125 ADPVGSSS--YEDTIPIDLVFNAFESFYGLRPMADDKIKFLEMNSIVDITIPTF 183
 DB 135 SNPIESCQNFKDDTLQIDMAFNFFLYFGLRPIANDKIMFLEVNSVDFETVPVF 194

QY 184 ISYLLKSNMGLRFLRALRLLELPQIILQILRAIKTSNSVKRSKLSLITSLTFTWPAAGFIH 243
 DB 195 VSVYLNRSWGLRFLRALRLIQESEILQFLNLIKTSIKLVNLSIFISWLTAAAGFIH 254

QY 244 LVENSGDPMWLGKRSQNSISYFESIYLVWATTSTVGFDVYAKTSIGRTIMEFTLGLSL 303
 DB 255 LVENSGDPMWENFQNNQALTYMECYLLMTVMTSTVGQDVYAKTTLGRLEWVEFTLGLGLAM 314

QY 304 FANIPPEWELFANKRKRTSSYEALKGKFTYVCGNITVDSVTFALRNFLDKSGEINTE 363
 DB 315 FASVPEPEIIEIGNRKKYGGSYSAVSGRKHLYVCGHITLESVSFLDFLKDDVDVAVE 374

QY 364 IVFLGETPPSLEETIEFKCYLAITYTFTSGSAMKEDLRVAVESAECILIANPLCSDSH 423
 DB 375 IVFLHNISPNLELALFKRHFTQVEFYQGSVLYNPHDLARVIESADACLIANKYCADPD 434

QY 424 AEDISNIMRVLSINVDSTRIIILQIASHNKVYLPKIPSNMMDGNIITCEAEKLGFI 483
 DB 435 AEDASNIMRVLSINVKHPKIRIITQMLQYHNKALHLPISNMKEGDALICLAEKLGFI 494

QY 484 AOGGLVGLCEFTLSFVEONKKVMPKQTMKHFLLNSKNNILQRLSDDFAGSFPPEVA 543
 DB 495 AOGSLAOGSLTMLANLFSMSRFIIEEDTMOKITLEGVSNEMTYEYLSAFAVGLSFPFVC 554

QY 544 RLCEFLKMYLLILIAIEYKSLFTDGCGLILNBPQVRIKNTLGEFIETPRVRALEFYC 603
 DB 555 ELCEVTKLKLMLIAIEYKSANRES--RLINPGNHLKIQEGFLGFASDAEVARAFPYC 612

QY 604 SVCHDDVPIPELITNCGCKSRSHQITVPSVKRKKCLGKISSKISGQDSPRVSASISS 663
 DB 613 KACHDDITDPRIKRCGCK--RLEDEQPSLSPRK-----KORNGGRNSP----- 656

QY 664 ISNFTTTLQHD-----VEDSDQLDSSGMFHWCKPSTLQDKVTLKRTGSKSKYK 711
 DB 657 --NTPSKLMRHDPILILIGNDQIDNNDNSVKKYDSTGMFHWCAPEIEIVILITRSAAATV 714

QY 712 FRNHIVACVFGDAHSAPWGLRNFYMPLRASNYTRKELDIYFISGLDYIQREMFRLNFP 771
 DB 715 LSGHVYVCIFEDVASALIGLNLVMPLRASNFHYHELKHIVFGSIEVLRKEMWELIHNFP 774

QY 772 QIYLLPGCALYSGLLHAANIEQCSKCAVLSPPOPSMQTLVDEALMATLTIGSLQID- 830
 DB 775 KVSILPGPIISRADLRVAINIMLCMVCYILSANQNNIDTSLQDEKCIASINIKSMOPDD 834

QY 831 -----SSSDPSPSVSE--ETPGYTNHGHNSKCRVPIITLKNPSN 870
 DB 835 SIGVLQANSQGFPPGMDRSSPDSVPHGMLRQPSITTVG-----IPITTELVDJTN 887

QY 871 IHFEIOGLGEGSLQETLHLSTAFSTGVSSFLDLSLTAAYNVHLLQMLVYGC 930
 DB 888 VQFLDQ---DDDDPDTFLYLTQFPACTAFAVSLDLSMATYFENDIILILIRLVYGC 944

QY 931 VSSOLEHLDKQYGVADSCSTLSLGRNCKLGLSLHETILSDVNRNFTGOLFCGSL 990
 DB 945 ATPLEALIAEENMLRGYSTPOTLANHRCRVAQLALLDGPFDLGDGCGYGLFCAL 1004

QY 991 DLFGIICVGLYRIDEEELNPE--NKRFTVTRPANEEKLPSDLVPCAFIPSTACYKRNE 1048
 DB 1005 KTYMMLCFGLYRLDAHLSPSQCTKRYVTYNPEFEVLPTDILFCMLQF----- 1055

QY 1049 EFSLOKSYEIVNKASQTTEDTFRRKLSHPL 1079
 DB 1056 DHNAGOSRALSHSHSSHQSSSKSSVHST 1086

RESULT 11
 Q9UOK6 PRELIMINARY; PRT: 1113 AA.
 AC Q9UOK6;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
 DE BKCA ALPHA SUBUNIT.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PULMONARY ARTERY;
 RA Cairns V.R., Aebly M.R., Rusch N.J.;
 RT "Cloning and Characterization of BKCA Alpha Subunit from Human
 RT Pulmonary Artery."
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF118141; AD31173.1; -
 DR Interpro: IPR000636; -
 DR Interpro: IPR002052; -
 DR Interpro: IPR003066; -
 DR Interpro: IPR003091; -
 DR Pfam: PF00520; Ion_trans. 1.
 DR PRINTS: PR00169; KCHANNEL.
 DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
 DR PROSITE: PS00092; N6_M7ASE; UNKNOWN_1.
 SQ SEQUENCE 1113 AA; 125181 MW; 17A9F6259731C31 CRC64;

Query Match 41.1%; Score 2354.5; DB 4; Length 1113;
 Best Local Similarity 43.4%; Pred. No. 2.2e-160;
 Matches 482; Conservative 196; Mismatches 329; Indels 105; Gaps 17;

QY 26 AFILSSVFTEFSGILILILIFRLIRSVK-KW-----QIIKGTGIIILEFTS 70
 DB 24 AFLASSVTFEFGGLFI-----LMRLTKYLMVTVCCHCGGKTEAKKINNGSS-----QAD 74

QY 71 GTI-----ARSHVRSJLHFOGQFRDHIEMLSAQTVEGQVLYLVFVLSIGSLIYFINS 124
 DB 75 GTLKPVDKEEAAVAEYGMWTSVKDMAGVMISAOTLTGRVLVYLVFALSIGALVIYFIDS 134

QY 125 ADPVGSSS--YEDTIPIDLVFNAFESFYGLRPMADDKIKFLEMNSIVDITIPTF 183
 DB 135 SNPIESCQNFKDDTLQIDMAFNFFLYFGLRPIANDKIMFLEVNSVDFETVPVF 194

QY 184 ISYLLKSNMGLRFLRALRLLELPQIILQILRAIKTSNSVKRSKLSLITSLTFTWPAAGFIH 243
 DB 195 VSVYLNRSWGLRFLRALRLIQESEILQFLNLIKTSIKLVNLSIFISWLTAAAGFIH 254

QY 244 LVENSGDPMWLGKRSQNSISYFESIYLVWATTSTVGFDVYAKTSIGRTIMEFTLGLSL 303
 DB 255 LVENSGDPMWENFQNNQALTYMECYLLMTVMTSTVGQDVYAKTTLGRLEWVEFTLGLGLAM 314

QY 304 FANIPPEWELFANKRKRTSSYEALKGKFTYVCGNITVDSVTFALRNFLDKSGEINTE 363
 DB 315 FASVPEPEIIEIGNRKKYGGSYSAVSGRKHLYVCGHITLESVSFLDFLKDDVDVAVE 374

QY 364 IVFLGETPPSLEETIEFKCYLAITYTFTSGSAMKEDLRVAVESAECILIANPLCSDSH 423
 DB 375 IVFLHNISPNLELALFKRHFTQVEFYQGSVLYNPHDLARVIESADACLIANKYCADPD 434


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Db 850 VNINLCDCVLLSANONNIDTSLDQKCEILASINIKSMQFDDSIGVLQANSQGFPPGM 909
Qy 831 --SSDPSVSE-ETPGYTNHNEKSNCRKVPITTELKNSNIHFITQDGLGEGSLQET 887
Db 910 DRSSDPSVSE-ETPGYTNHNEKSNCRKVPITTELKNSNIHFITQDGLGEGSLQET 959
Qy 888 NLHSTAFTGTGVSSPSSSLATAFYNYVLELLQMLTVGVSSQLEQHLDDKQVGV 947
Db 960 ELYLTPPACGTAFAYSLDLSMSTYFNNDILIRLTVGATPELEALAEENALRG 1019
Qy 948 ADSCSLISGRNCKLGLSLHETILSDVNPRTFGQLFCGSLDFGLICVGLRIIDE 1007
Db 1020 GYSTPOTLANDRCRVALDLDGFDLGDGCGDLCFKALKTYNMCEGIYRLDAH 1079
Qy 1008 ELNPE--NKRFRITRPAEFLLPSDLVFCALPSTACRYKNEEFLQKSYEIVKASOT 1065
Db 1080 LSTPQCTKRVITNPPREFELVPTDLFCIMQF-----DHNAQOSRASLSHSSHS 1130
Qy 1066 TEDFRHKLSSHPL 1079
Db 1131 SSSSSKSSSVHST 1144

RESULT 13
018866 PRELIMINARY: PRT: 1152 AA.
ID 018866
AC 018866:
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE CALCIUM-ACTIVATED POTASSIUM CHANNEL ALPHA SUBUNIT.
OS Sus acrota (P19).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
OX NCBI_TaxID=9623;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LENS EPITHELIUM;
RA Rae J.L., Shepard A.R.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF026000; AAB88803.1; -.
DR InterPro; IPR000636; -.
DR InterPro; IPR001622; -.
DR InterPro; IPR002052; -.
DR InterPro; IPR003006; -.
DR Pfam; PF00520; Ion_Ctrans; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR PROSITE; PS00092; N6_MTASE; UNKNOWN_1.
KM Ionic channel.
SQ SEQUENCE 1152 AA; 128988 MW; D62C91963D60ADBC CRC64;
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Query Match 41.1%; Score 2351.5; DB 6; Length 1152;
Best Local Similarity 43.0%; Pred. No. 3.8e-160;
Matches 485; Conservative 195; Mismatches 345; Indels 103; Gaps 17;
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Db 271 SIKLVNLSIFSTWLTAGFIHLVPEGDPWENQNNQALTYEVCYLLWMTSTVYG 330
Qy 281 DVYAKTSLGRFFIMFTGLSILFANTYPEWELEPANKRKTSSYEALKKFIVCGNI 340
Db 331 DVYAKTSLGRFFIMFTGLSILFANTYPEWELEPANKRKTSSYEALKKFIVCGNI 390
Qy 341 TVDSYATFLNRLKSGEINTEIVFGETPPSLELEIFCYLAVTTFISGAMKMDL 400
Db 391 TVDSYATFLNRLKSGEINTEIVFGETPPSLELEIFCYLAVTTFISGAMKMDL 450
Qy 401 RRVAVESAELILIANPLCSDSHAEDISINIRVLSIKNYDSTTRITIOILOSHNVYLPK 460
Db 451 ARVKIESADACILIANKCAPDAEDASINIRVLSIKNYDSTTRITIOILOSHNVYLPK 510
Qy 461 IPSNMWDTGNITICPAELKLFIAOGCLVPGCLFVLSFVYBONKVPKOTWKKHFLNS 520
Db 511 IPSNMWDTGNITICPAELKLFIAOGCLVPGCLFVLSFVYBONKVPKOTWKKHFLNS 570
Qy 521 MNKRLTQRLSDDFAGMSFEPVARLCFLKMYLLITALEYKSLFTDGFGLINPPQVRI 580
Db 571 VSNEMTEYLSAFVGLSEFVYCELFVYKLLMLAIEYKSNRRES--RIILNFGNHLKI 628
Qy 581 RKNLTGFFIAETPKDVRALFYCSYCHDVFPELITNCGCKSRQHIITVSVKRMKCK 640
Db 629 QEGTLGFFIADAKKVRKAFYCKACHDITDPKRIKKCGCK--RLDEQPSLTSPKKK 685
Qy 641 LKGISSRISGDDSP-----PRVSASTSSISNFTTRITQHDVEDSDQLDSSGFHWCKP 694
Db 685 LKGISSRISGDDSP-----PRVSASTSSISNFTTRITQHDVEDSDQLDSSGFHWCKP 736
Qy 694 QNGMGRNPSPPSLMRHBDLLTPGNDQIDN-----MDSVVKVYDSTGFMHWCAP 736
Db 736 QNGMGRNPSPPSLMRHBDLLTPGNDQIDN-----MDSVVKVYDSTGFMHWCAP 754
Qy 754 TSLDVTLKRTGKSKYKFRNHIYACVFGDAHSAPKGLRNFMPLRASVYTRKELDIYFI 754
Db 754 TSLDVTLKRTGKSKYKFRNHIYACVFGDAHSAPKGLRNFMPLRASVYTRKELDIYFI 796
Qy 797 KEIEVILTRSEAMTVVSGHYVVICFQDVSSALIGLNLVMPLRASFHHELKHIYFV 796
Db 797 KEIEVILTRSEAMTVVSGHYVVICFQDVSSALIGLNLVMPLRASFHHELKHIYFV 814
Qy 815 TSLDVTLKRTGKSKYKFRNHIYACVFGDAHSAPKGLRNFMPLRASVYTRKELDIYFI 814
Db 815 TSLDVTLKRTGKSKYKFRNHIYACVFGDAHSAPKGLRNFMPLRASVYTRKELDIYFI 856
Qy 856 TSLDVTLKRTGKSKYKFRNHIYACVFGDAHSAPKGLRNFMPLRASVYTRKELDIYFI 856
Db 856 TSLDVTLKRTGKSKYKFRNHIYACVFGDAHSAPKGLRNFMPLRASVYTRKELDIYFI 914
Qy 857 KEIEVILTRSEAMTVVSGHYVVICFQDVSSALIGLNLVMPLRASFHHELKHIYFV 914
Db 857 KEIEVILTRSEAMTVVSGHYVVICFQDVSSALIGLNLVMPLRASFHHELKHIYFV 914
Qy 854 SNCRKVPITTELKNSNIHFITQDGLGEGSLQETNLHSTAFTGTGVSSPSSSLATA 913
Db 913 SNCRKVPITTELKNSNIHFITQDGLGEGSLQETNLHSTAFTGTGVSSPSSSLATA 966
Qy 915 -----IPITTELVDNTNQFIDQ--DDDDPDELYLTQPACTAFAYSLDLSMSAT 966
Db 966 -----IPITTELVDNTNQFIDQ--DDDDPDELYLTQPACTAFAYSLDLSMSAT 973
Qy 914 FYNVHLELLQMLTVGVSSQLEQHLDDKQVGVADSCSTSLSGNRCKLGLSLHETIL 973
Db 973 FYNVHLELLQMLTVGVSSQLEQHLDDKQVGVADSCSTSLSGNRCKLGLSLHETIL 1026
Qy 967 YFNDNILLIRLTVGATPELEALAEENALRGYSTPOTLANDRCRVALDLDGDF 1026
Db 1026 YFNDNILLIRLTVGATPELEALAEENALRGYSTPOTLANDRCRVALDLDGDF 1086
Qy 1032 LVEFCAIPSTACRYKNEEFLQKSYEIVKASQTFEDFRHKLSSHPL 1079
Db 1086 LVEFCAIPSTACRYKNEEFLQKSYEIVKASQTFEDFRHKLSSHPL 1125

RESULT 14
008460 PRELIMINARY: PRT: 1196 AA.
ID 008460
AC 008460: 064703;
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE SLOWPOKE HOMOLOG. POTASSIUM CHANNEL, CALCIUM-ACTIVATED (CALCIUM-
DE ACTIVATED POTASSIUM CHANNEL) (SLOWPOKE HOMOLOG PROTEIN).
CN KCMNA1 OR SLO.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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[illegible]

	Score	DB 11, Pred. No. 5.1e-160;	Length 1196;
Query Match	41.18;		
Best Local Similarity	42.68;		
Matches 483; Conservative	198; Mismatches 341;		
		Indels 112;	Gaps 17,

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0Y      15 PKMSC-----TTEIOA-----AFISSFVTFEFGSILLIFRLIMRSVK-KMOII- 58
      ||      |      |      |      |      |      |      |      |      |
Db      26 PKMDLIIPVMEVPCDSRGORMMMAFLASSMYTFEFGSLFI-----LLMRKLKLMVCC 81
0Y      59 -----KGTGIIILEFTSGTIANSHVRSLHFGOCFDRHIMLSAOTFV 101
Db      82 HCGGKTKEAOKINNGSSQADETLKPVEDEKEVVAEV---GMMTSVMDMACVMISAOTLT 138
0Y      102 GOVLITLIVFVLSIGSLIIVFINSDDPVGSSS-YEDKTRIPIDLAFNAPFSFPELIRMAA 160
Db      139 GRVLVWLFALSIGLAVLYIFIDSSNPDESCONFKDFTLOIDMAFNFFLLYFELRLTAA 198
0Y      161 DDKIKFMLEMNSIYDIETIPPTFISLYLKSWMGLRFLRALRLLELPOIILQILRAIKTSN 220
Db      199 NDKLMEFMEVNSYVDFEIVPPVPSVYINRSWGLRFLRALRLLOFSSILQFLMILWTSN 258
0Y      221 SVKSSKLSLILSTWFTWAGTILHLVENSGBPWLKGRNSQNI SYESYSILVMATTSVWG 280
Db      259 SIKLWNLSIFISWTWTFAGTILHLVENSQDPMENFOONQALTYECVYLLMTVMTSTVGYG 318
0Y      281 DVVATSLSGRFMEFTGSLILFANYPENVELFANKRKRTTSYELAKKKFTVYCGNI 340
Db      319 DVYATYTLGRLFPMVFFILGGLAMFASVYPELTIELIGNKKTKGGSYSAVSGKHVYCGHI 378
0Y      341 TVDSYTAFLRNLBRDKSGEITELTEVFLGCEPSPSELETIFKCYLAATYTFIGSMMKMEDL 400
Db      379 TLESVSNLKFPLKRDNDVAVELVFLHNISPNLELELFRHRHTYVBEFVGSVLANHDL 438
0Y      401 RRVAVESACLILIANPLCSDSHAEDISNIRVLISKNYDSTTRITIIQILOSNNKYVLPK 460
      ||      |      |      |      |      |      |      |      |      |

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Db	439	ARKVIESADACILLANTKCCADPPRAEDASNMRIYSIKNTNPKRITITQIMQYHNKHAHLN	498
Qy	461	IPSNMNDGDNICIEAELKGLFIAQCGVLPGCTLTSLFVEONKVKVMPKQTKMKHPLNS	520
Db	499	IPSNMNEGDDALICLALKGLFIAQSCLOAGSLTLMANLFMSKSFIIKEEDTWQYLEG	558
Qy	521	MKNLILQRLSDPADGSPPEVVARLFCFLKYLILNIAIEKLSLTDFGCLLNPPQVRI	580
Db	559	VSNEMTEYLSAFAVGSFTYVCELCFVAKILMLAIEKSNANRES--RILNPGNHLKI	616
Qy	581	RKNTLGFETPDKVRAALFYCSVCHDVYFIPELLTNGCCKSRSRKHITVPSVKRMKC	640
Db	617	QEGTLGFEFISDAEYKRAFFCYKACHDVTDPKRKKCGCRRLIYFEEDEQPTLSPKK-	675
Qy	641	LKGSSISLISGDDSPRRSASATSSISNFTTRTLOH-----VQDSDDQISGGM	688
Db	676	-----KORNGGRNSP-----NTSPKLMHDDLPIPGNDQIDNMDSNKKTKDSTGM	721
Qy	689	FHWCKPTSLDKVTLKRTGSKSKYFRNHIYACVGDASHAPGLRNFVMPLRASANTREL	748
Db	722	FHWCAPIKEIKVILTRSEALMTVLGSHVYVCIGGDVSSALIGRLNVLMPLRASNFYHEL	781
Qy	749	KDIYFISLDYLQREKMFLLNFPQIYILRGCALYSDDLHAANIEQCSMCVAVLSPPROSS	808
Db	782	KHIVFVGSIIEYLRKHEMETLNFPRKVSILPOTPLSRADLRVAININLCMDKVIISANQNNID	841
Qy	809	NOTLVDPDEAMATLTISLQID-----SSSDPSVSVE-ETPGYT	847
Db	842	DTSLQDNECILASINIKSMQFDDISIGLVANSQGTFRPMDDSSPNSVNHMLRQPSIT	901
Qy	848	NGHNEKSNCRKVPITVELKNPSNIHPTLEQLGLESSLQETNLHLSTAFSTGVTFSSFLD	907
Db	902	TGVN-----IPITTELVDNTVQVFLDQ---DDDDDDPTTELYLTPQFACGTAFAVSYLD	951
Qy	908	SLTATAFYNYHVELLQMLVTGVSQSLQEDHDKDKVUYGVAUSDCTSLSGNRCKLTGLS	967
Db	952	SLMSATTFVNDNIILTLITVLTGCGATEPELMLAEEBALGCGSTROTLLANRRCVQAOLA	1011
Qy	968	LHETILSDVNRNPFQGLFCGSLDLFGILCVGLRIIDEELNPE--NKRFEVITPRANEF	1025
Db	1012	LLDPPFADLGGCGCGDLPFCALKATYNNMLCFGIYRLDANHLSTPSCGTARYVITNPREF	1071
Qy	1026	KLLESDILVFCALIPRSTACRYRNEEFSLOKSYELVNKASQTTEDTFRHKSSHPL	1079
Db	1072	ELVPTFDLIFCLMOP-----DHNAGGSRASLSHSSSQSSKSSVHST	1116
RESULT 15			
Q98951	ID	PRELIMINARY; PRT: 1118 AA.	
098951	AC	01-FEB-1997 (TREMblrel. 02, Created)	
098951	DT	01-FEB-1997 (TREMblrel. 02, last sequence update)	
01-OCT-2000	DT	(TREMblrel. 15, last annotation update)	
CALCIUM-ACTIVATED POTASSIUM CHANNEL.	DE		
Gallus gallus (Chicken).	OS		
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	OC		
Archosauilia; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;	CC		
Gallus.	CC		
NCBI_TaxID=9031;	OX		
(1)	RN		
SEQUENCE FROM N.A.	RP		
SPRAIN-WHITE LEGHORN; TISSUE=BRAIN.	RC		
Rosenthal K.P., Hudspeth A.J.;	RA		
Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.	RL		
EMBL: U73189; AAB17873.1; -	DR		
InterPro: IPR000636; -	DR		
InterPro: IPR001622; -	DR		
InterPro: IPR002052; -	DR		
InterPro: IPR003006; -	DR		
Pfam: PF00520; Ion_trans. 1.	DR		
PROSITE: PS00290; IG_MHC; UNKNOWN.1.	DR		
PROSITE: PS00092; N6_MTASE; UNKNOWN.1.	DR		

KW Ionic channel.
SQ SEQUENCE 1118 AA: 125843 MW: 535DA3DBAE87A47 CRC64:

Query Match 41.18; Score 2349.5; DB 13; length 1118;
Best Local Similarity 44.08; Pred. No. 5.1e-160;
Matches 487; Conservative 183; Mismatches 349; Indels 89; Gaps 16;

26 AFISSPVTFPSGLIILIFRLIMRSVK-KW-----QIINGTGIIIELEFISG 71
24 AFLASSNVTFFGGLEFI---LNMRTLYLMTVCCHCCKKKEAKIKGG---DTQADG 76
72 TIARSHVR-----SLHFQGFQRDHLEMLSAQTFVGQVILVEVLSIGSLIYFINS 125
77 ACKPTDEKEENVAAEVGMVTSKDMAGVISAQTLTGVLVVLVAFALSIGALVIFIDSS 136
126 DPGVSCSS-YEDKTIPIIDLVNAPFSPFGURFMAADKIKFMLEMNSIVDIFIPPTFI 184
137 NPISCONFYKDFLQIDMAFNVEFLYFGRLFAANDKLMFMLEVNSVDFEIVPPEV 196
185 SYLKSNNLGLRFLRALRLLELPOLILRAIKTNSVSKFSKLSLIISTWETAAGFTHL 244
197 SVYLNRSWLGRLRLALRLIOFSELIOFLNLTKTSNLIKLVNLCSTFTWLTAGFTHL 256
245 VENSQDPMKGRNSQNSISYFESIYLVNATSTVGEGDVAAKTSIGRTIMEFTIGSLILF 304
257 VENSQDPMENQNNQOLTWECYVLLAMWTMGVGDYAKTTLGRLFMVFILGGLAMF 316
305 ANYIPENVELFANKRKYTSSEALKGKKEIYVCGNIVDSVTAFLNFLRDKSGEINTEI 364
317 ASYVPEIIEILGNRKKGYSYSAVSGRKHIVCGHITLESVNFLEKDFLHKDRDDVNEI 376
365 VFLGETPSLELIEFCKYLAFTTFISSAMKWEDELRYVAESAACLIITANPLCSDSHA 424
377 VFLNINISPNLELALFKHFTQVEYQSVLPHDLARVKTIESADACILANKKICADPDA 436
425 EDISINMRVLSIKNVYDSTRIIIOILOSNNKVVLPKIPSNMMDGDNITCFEALKGFLA 484
437 EDASINMRVISIKNVHPKIRITQMLQYHNKNAHLNIPSNMKEGDDAICLAELKGFLA 496
485 QGCLVPGICLFTLSEFQONKKVMPKOTKKHFLNSMKNKILTORLSDDFAGMSFEVAR 544
497 QSC LAPGISTMLANLFMSRSEFIKIEEDTWQKYLEGVANEMYTELSSAFVGLSEPAVCE 556
545 LCFLEKMYLLAIEYKSLFTDGF--GLINPPQVIRKNTLGFETAEPTKDVRALEY 602
557 LVFAKLMLLTAIEYKSEKRSRKRRLINPGNHVKIQEGTLGFFLASDAKEVARAFY 616
603 CSVCHDVFIFELITNCGCKSRSRQHTVPSVKRMKCKLKGISRSISGQDSP-----PR 656
617 CKACHDDITDPKRIKKCGCK---RLEDQPTSLSPKKKQNGMGMRNSPNSPKLMRHDP 673
657 VSATSSISNFTTTLQHDVEQDSQDLSGFMHCKPTSLDKVTLKRKGSKKYEKNHI 716
674 LIPNEQIDN-----MDANVKKYDSTGMFWCIPAKDIEKYLITRSEAMVLSGHV 724
717 VACVGGDAHSAPMGRNFVMPFLRASNYTRKELKDIYFISLDYLOREWRFLRNFOIYL 776
725 VVCIFGDKYKSLIGRLNLYMPLRASNFHYHEKHLVFGSLLEYLRREWETLHNEPKVSIL 784
777 PGCALYSGDLHAANIEOCSMCVAVLPPQPSNQTLVDTAEMATLTIGSLQID----- 830
785 PGTPLSRADLRAVININLCDMCVILSANQNNIDASLQDECIASLNKISMQFDDSIGVL 844
831 -----SSSPSPSPSVS-EETPGYTNGHNEKSNCRKVPILTELKNSINHFIE 875
845 QANSQGFPPGMDSRSPDSSPVHGLLRQPSITTGAN-----IPITELVNDSSNVQFLD 897
876 QUGGLESLQETNLHLSTAFNGVTFSSFLDSLATAFYNVHYELLOMLVTGGVSSOL 935
898 Q-----DDDDPPTLELITQPFACGTAFVAVSDLSMSATYFENDNIIITLITLVGATPEL 954
936 EOHLDKDKVYGVADSCSTLSLGRNCKLGLLSLHETILSDVNPRTFQGLFCGSLDLFGI 995

1046 RNEEESLQKSYEIVNKKASQTEDETFRRHK 1073
1075 SHSSYSSKSSSVHSTPSTANRRNRK 1102

Search completed: October 5, 2001, 12:14:27
Job time: 629 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 5, 2001, 12:12:21 ; Search time 29.2 Seconds

(without alignments)
1296.312 Million cell updates/sec

Title: US-09-176-664-16

Perfect score: 5722
Sequence: 1 MFQTKLRNETMEDLPKMSCT.....CINQSILTSRELTPLSLK 1105

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 3425486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	ID	Description
1	216.5	3.8	209	1	Y139_METJA	Q57603 methanococ
2	162	2.8	806	1	CIKB_CANFA	Q95167 canis fam1
3	158.5	2.8	853	1	CIKA_RAT	P15387 rattus norv
4	158.5	2.8	854	1	CIKA_HUMAN	Q14721 homo sapien
5	158	2.8	802	1	CIKB_RAT	Q63099 rattus norv
6	157	2.7	924	1	CIKB_DROME	P17970 drosophila
7	154.5	2.7	806	1	CIKB_HUMAN	Q92953 homo sapien
8	147	2.6	499	1	CIK2_HUMAN	P15389 homo sapien
9	144	2.5	499	1	CIK2_MOUSE	P15386 mus musculu
10	144	2.5	499	1	CIK2_XENLA	P22739 xenopus lae
11	143.5	2.5	433	1	YD57_METJA	Q58752 methanococ
12	143.5	2.5	676	1	CIQ1_HUMAN	P51787 homo sapien
13	140	2.4	604	1	CIQ1_MOUSE	P97414 mus musculu
14	139.5	2.4	643	1	CIK2_DROME	P08511 drosophila
15	139.5	2.4	656	1	CIK2_DROME	P08513 drosophila
16	139	2.4	691	1	TKO1_YEAST	P40310 saccharomyc
17	138.5	2.4	616	1	CIK1_DROME	P08510 drosophila
18	136	2.4	757	1	CIKE_HUMAN	Q14003 homo sapien
19	135.5	2.4	490	1	CIKL_DROME	P17971 drosophila
20	135	2.4	889	1	CIKE_RAT	Q01956 rattus norv
21	133	2.3	769	1	CIKE_MOUSE	Q63959 mus musculu
22	133.5	2.3	1174	1	CIKE_DROME	Q02280 drosophila
23	131.5	2.3	498	1	CIK1_DROME	P17972 drosophila
24	131.5	2.3	1032	1	MT18_YEAST	P40469 saccharomyc
25	131	2.3	638	1	CIKE_RAT	P22462 rattus norv
26	131	2.3	872	1	CIQ3_HUMAN	Q45525 homo sapien
27	129.5	2.3	2164	1	POLG_HRB9	P07210 human rhino
28	129	2.3	1581	1	AROL_PNECA	Q12659 p pentaculo
29	125.5	2.2	528	1	CIK3_MOUSE	P16390 mus musculu
30	123	2.1	417	1	KCH_ECOLI	P31069 escherichia
31	122.5	2.1	523	1	CIK3_HUMAN	P22001 homo sapien
32	122.5	2.1	525	1	CIK3_RAT	P15384 rattus norv
33	121	2.1	530	1	CIK6_RAT	P17659 rattus norv

34	120.5	2.1	511	1	CIKD_HUMAN	P48547 homo sapien
35	120.5	2.1	511	1	CIKD_MOUSE	P15388 mus musculu
36	120.5	2.1	585	1	CIKD_RAT	P25122 rattus norv
37	120.5	2.1	1001	1	ORL1_DROME	Q94526 drosophila
38	120	2.1	2171	1	CCAC_RABIT	P15381 oryctolagus
39	118.5	2.1	902	1	POLG_PVYN	Q14053 schizosacch
40	118.5	2.1	3063	1	YC47_SCHPO	P18247 p genome po
41	117.5	2.1	541	1	NU5M_ARTSF	Q37710 artemisa san
42	117	2.0	495	1	CIK1_HUMAN	Q09470 homo sapien
43	117	2.0	695	1	CIQ4_HUMAN	P55696 homo sapien
44	116.5	2.0	495	1	CIK1_MOUSE	P16388 mus musculu
45	116.5	2.0	495	1	CIK1_RAT	P10499 rattus norv

ALIGNMENTS

RESULT 1
ID Y139_METJA STANDARD: PRT: 209 AA.
AC Q57603:
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE HYPOTHETICAL PROTEIN MJ0139.
GN MJ0139.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
OC Methanococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.F., Adams M.D., Reisch C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Uitterback L.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser K.M., Smith H.O., Weese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
jannaschii.";
RL Science 273:1058-1073(1996).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC -1- SIMILARITY: SOME TO POTASSIUM CHANNEL PROTEINS.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: U67471; AAB98122.1; -
DR TIGR: MJ0139; -
DR InterPro: IPR000636; -
DR Pfam: PF00520; Ion_Trans_1.
KW Hypothetical protein; Transmembrane.
FT TRANSMEM 11
FT TRANSMEM 72
FT TRANSMEM 126
FT TRANSMEM 157
FT TRANSMEM 182
FT TRANSMEM 202
SQ SEQUENCE 209 AA: 24183 MW; FC91E7320F34D90F CRC64;

Query Match 3.8%: Score 216.5; DB 1; Length 209;
Best Local Similarity 25.9%; Pred. No. 1.4e-07;
Matches 60; Conservative 55; Mismatches 80; Indels 37; Gaps 7;

QY	103	QVLTVLVLVSLSGSLIIFINISADVSCSSDEDITPDVFNFNFFSFLRPMADD	162
Db	10	KIMELVSLIFPEIYASFLSTYN-----PYQDLIKNDIYSIMFFFEIYNYVED	64
QY	163	KIKFVLENNISVDITPTPTISYLK-----SNWGLRFLRALRLLELPQILQILRAKT	218
Db	65	KAKFPRDYNIVDAIV--IAFLVLSQVFNYSKAFGLRYINLRILVLRIRIKRKLEEN	123
QY	219	SNSVFESKLSTILSTWTFAGFHLVNSGPGWPKGRNSQISVFEESLYLMATSTWG	278
Db	124	QALINEFLTLTIC-----FLASCLIVIVSGVNPAIN-----NFDVFFYTTISITTVG	172
QY	279	FQDVVAKTSLGRTFTIMEFTLGLILFANVIEPMELFANKRKYTSYSEALG	330
Db	173	YGDIPKPTDAGKLRIIF-----SVLFEISGL-----ITSLSQALKG	208
RESULT	2		
CIKB_CANFA	STANDARD;	PRT;	806 AA.
AC	Q95167;		
DT	15-JUL-1999 (Rel. 38, Created)		
DT	15-JUL-1999 (Rel. 38, Last sequence update)		
DE	15-JUL-1999 (Rel. 38, Last annotation update)		
GN	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV2.2.		
OS	KCNB2.		
OC	Canis familiaris (Dog).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.		
OX	NCBI_TaxID=9615;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=98275219; PubMed=9612272;		
RA	Schmaltz F., Kinseila J., Koh S.D., Vogalis F., Schneider A.,		
RA	Flynn E.R., Kenyon J.L., Horowitz B.;		
RT	"Molecular identification of a component of delayed rectifier current		
RT	in gastrointestinal smooth muscles.";		
RL	Am. J. Physiol. 274:G901-G911(1998).		
CC	-I- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM		
CC	ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED		
CC	CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE		
CC	MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH		
CC	WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL		
CC	GRADIENT.		
CC	-I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.		
CC	-I- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE SENSOR AND IS		
CC	CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT		
CC	EVERY THIRD POSITION.		
CC	-I- DOMAIN: THE TAIL MAY BE IMPORTANT IN MODULATION OF CHANNEL		
CC	ACTIVITY AND/OR TARGETING OF THE CHANNEL TO SPECIFIC SUBCELLULAR		
CC	COMPARTMENTS.		
CC	-I- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER		
CC	CLASS. BELONGS TO SHAB POTASSIUM CHANNEL SUBFAMILY.		
CC	-----		
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CC	use by non-profit institutions as long as its content is in no way		
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/		
CC	or send an email to license@isb-sib.ch).		
CC	-----		
DR	EMBL; U69963; AAB08432.1; -		
DR	InterPro: IPR000636; -		
DR	InterPro: IPR003091; -		
DR	Pfam; PF00520; Ion_Trans; 1.		
DR	PRINTS; PF00169; KCANANNEL.		
KW	Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;		
KW	Glycoprotein; Multigene family; Phosphorylation.		
FT	DOMAIN 1 190 CYTOPLASMIC (POTENTIAL).		
FT	TRANSMEM 191 212 SEGMENT S1 (POTENTIAL).		
FT	DOMAIN 213 232 EXTRACELLULAR (POTENTIAL).		
FT	TRANSMEM 233 254 SEGMENT S2 (POTENTIAL).		

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FT DOMAIN          255   264      CYTOPLASMIC (POTENTIAL) .
FT TRANSEM        255   286      SEGMENT S3 (POTENTIAL) .
FT DOMAIN         287   298      EXTRACELLULAR (POTENTIAL) .
FT TRANSSEM       299   320      SEGMENT S4 (POTENTIAL) .
FT DOMAIN         321   334      CYTOPLASMIC (POTENTIAL) .
FT TRANSEM        335   356      SEGMENT S5 (POTENTIAL) .
FT DOMAIN         357   396      EXTRACELLULAR (POTENTIAL) .
FT TRANSEM        397   418      SEGMENT S6 (POTENTIAL) .
FT DOMAIN         419   806      CYTOPLASMIC (POTENTIAL) .
FT CARBOHYD       287   287      N-LINKED (GLCNAC...) (POTENTIAL) .
SQ SEQUENCE       806 AA;    90283 MM; D962EC236760B743 CRC64;

Query Match             2.8% ; Score 162; DB 1; Length 806;
Best Local Similarity 22.8%; Pred. No. 0.0041;
Matches     63; Conservative 62; Mismatches 109; Indels 42; Gaps 8;

QY 88 RDHIELLSAQTEVNGOVLIVLVEFLSTGSLIIYFINSADPVGGSSSY----EDKTIID 142
DB 180 RDLLEKPNS--SVAKILAIYSNLFYSTIALSINTPELDQEMDEFOPNDPOLAHVE 237
QY 143 LVFNAAFEFYGCGRPMADDKKIKFMLENMSVVDFPTTPPTSIVYL-KSNMLGLFRAL 201
DB 238 AVCAAMFWMEILLNFLRFLSPKNWKFKGPLANVIDLAIIIPLYVTIFLTSSNKSVLOFOVR 297
QY 202 RLDELPOQLIOLRAIKTSNV-----FKSKLLSIILTWTFTAAG---FIH 243
DB 298 RVVOIFIIRIMRLRIKLKHSHSTGLSGTLRTSRSENEIGLIIT--ETAMIMIFFSLVF 354
QY 244 LVENSGDPWLKGNRSNQNTSFESJLYVAATSTVGFGGVNAKTSLGRFINFPFLGSLL 303
DB 355 FAEKDADA-----TKFLTISPFASFWMATTMTTGYGDIITYKRILIIGKSVDGLCTIAGLV 408
QY 304 FANYIPENWEIFA-----NKRYTSSYEALKCKRK 332
DB 409 IALPIPIVPPEFSFYKEQRQEKAIRKERALERAK 444

RESULT 3
CIRK_RAT ID CIRK_RATE STANDARD; PRT; 853 AA.
AC PI5387;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV2.1 (DRKI).
OS RATUS NORVEGIENS (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OX Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN NCBI_Taxid=10116;
[1]
RN SEQUENCE FROM N.A.
RC TISSUE-BRAIN:
RP MEDLINE=89365157; PubMed=2770868;
RX Frech G.C., Vandongen A.M.J.; Schuster G.; Brown A.M.; Joho R.H.:
RT "A novel potassium channel with delayed rectifier properties isolated from rat brain by expression cloning.";
RL Nature 340:642-645(1989).
[2]
RN REVISIONS.
RP RA Frech G.C.;
CC Submitted (FEB-1990) to the EMBL/GenBank/DDBJ databases.
CC -!- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
CC CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
CC GRADIENT.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: IN THE BRAIN, THE GREATEST DENSITY OCCURS IN
CC THE CEREBRAL CORTEX, FOLLOWED BY THE HIPPOCAMBUS, CEREbellum, AND
CC OLFACTORY BULB. IN PERIPHERAL TISSUES IT IS MOST PROMINENT IN
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CC RETINA AND KIDNEY. ALSO PRESENT IN CARDIAC MUSCLE TISSUE OF THE
CC ATRIUM AND VENTRICLE AND IN SKELETAL MUSCLE.
CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION.
CC -1- DOMAIN: THE TAIL MAY BE IMPORTANT IN MODULATION OF CHANNEL
CC ACTIVITY AND/OR TARGETING OF THE CHANNEL TO SPECIFIC SUBCELLULAR
CC COMPARTMENTS.
CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
CC CLASS. BELONGS TO SHAB POTASSIUM CHANNEL SUBFAMILY.
CC -----
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CC -----
DR EMBL: X16476; CAA34497.1; -.
DR PIR: S05448; CHRPD1.
DR InterPro: IPR000636; -.
DR InterPro: IPR003091; -.
DR Pfam: PF00520; Ion_trans; 1.
DR PRINTS: PR00169; KCHANNEL.
KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KM Glycoprotein; Multigene family; Phosphorylation.
FT DOMAIN 1 182
FT TRANSMEM 183 204
FT TRANSMEM 205 224
FT TRANSMEM 225 246
FT DOMAIN 247 256
FT TRANSMEM 257 278
FT TRANSMEM 279 290
FT TRANSMEM 291 312
FT DOMAIN 313 326
FT TRANSMEM 327 348
FT DOMAIN 349 388
FT TRANSMEM 389 410
FT DOMAIN 411 853
FT CARBOHD 279 440
FT MOD_RES 440 440
FT MOD_RES 492 492
FT MOD_RES 95280 MM; 7A08998839716165 CRC64;
SO SEQUENCE 853 AA; 95280 MM; 7A08998839716165 CRC64;

Query Match 2.8%; Score 158.5; DB 1; Length 853;
Best Local Similarity 22.6%; Pred. No. 0.0075;
Matches 65; Conservative 64; Mismatches 123; Indels 35; Gaps 8;

OY 103 QVVLIVLVLSGLIIFINSADVGSSESTEDT-----IPIDLVFAFSPFGRLF 157
DB 185 KILALISIMFYLSLSTIALSLNLPQLSDERGSTDNPOLAHVAVCAMTMEYLAIF 244
OY 158 MAADKIKFMLEMNSIVDFITPFIISYLL-KSNMGLRRLRLRLPOLIOLRLAI 216
DB 245 LSSPKKMKFFKPLNAIDLLALPLFYVIFLTESKSVYGFONRVYOIFIMRLRL 304
OY 217 KTSNSVKFSKLSLILSTWETAAGFIHLVENSQDPLK-----GRNSONISYFESI--- 267
DB 305 KLARSTGLQSLGFTLRSYNELGLLFLWAGIMIFSLVFAEKDEDDTKFSIPASF 364
OY 268 YLVAMTSTVGCGDVVATSLGRTIMFTYGLSLFLFANYIEMELPA-----NKRK 320
DB 365 WMAITMTVTGGDILYPTLLGKIVGLCCIAGVLAIPILIVNNSEFYKEQROEK 424
OY 321 YTSSEALKGKFIYVCGN---ITVDSYTAFLR-----NFLRDKSGE 359
DB 425 AKRREALEPRAK-----RNGSIVSNMKMDAFARSIEMMDIYERKGE 466
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RESULT 4
CICKA_HUMAN STANDARD: PRT: 854 AA.
AC Q14721;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV2.1 (DHK1).
GN KCB1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid:9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Ikeda S.R., Soler F., Zuhke R.D., Joho R.H., Lewis D.L.;
RL Submitted (JAN-1993) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSURING OPENED OR CLOSED
CC CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
CC MEMBRANE. THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
CC GRADIENT.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION.
CC -1- DOMAIN: THE TAIL MAY BE IMPORTANT IN MODULATION OF CHANNEL
CC ACTIVITY AND/OR TARGETING OF THE CHANNEL TO SPECIFIC SUBCELLULAR
CC COMPARTMENTS.
CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
CC CLASS. BELONGS TO SHAB POTASSIUM CHANNEL SUBFAMILY.
CC -----
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CC -----
DR EMBL: L02840; AAA36156.1; -.
DR MIM: 600397; -.
DR InterPro: IPR000636; -.
DR InterPro: IPR003091; -.
DR Pfam: PF00520; Ion_trans; 1.
DR PRINTS: PR00169; KCHANNEL.
KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KM Glycoprotein; Multigene family; Phosphorylation.
FT DOMAIN 1 182
FT TRANSMEM 183 204
FT TRANSMEM 205 224
FT TRANSMEM 225 246
FT DOMAIN 247 256
FT TRANSMEM 257 278
FT DOMAIN 279 290
FT TRANSMEM 291 312
FT DOMAIN 313 326
FT TRANSMEM 327 348
FT DOMAIN 349 388
FT TRANSMEM 389 410
FT DOMAIN 411 854
FT MOD_RES 440 440
FT MOD_RES 492 492
FT MOD_RES 95521 MM; 360DEB3E45731EDA CRC64;
SO SEQUENCE 854 AA; 95521 MM; 360DEB3E45731EDA CRC64;

Query Match 2.8%; Score 158.5; DB 1; Length 854;
Best Local Similarity 22.6%; Pred. No. 0.0075;
Matches 65; Conservative 64; Mismatches 123; Indels 35; Gaps 8;
```

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OY 103 QVLIVLVLVLSIGSLIYFINSADPVGSCSYEDKT-----IPDLVFNAFESFYEGLR 157
DB 185 KILAIISIMFVLSLSTALSLNTLPELOSLDEFSGSTDPNOLAHVAVCIAFMFMEYLRF 244
OY 158 MAADKIKFMLEMNSIYDIFIPPTFISYLL-KSNMGLRFLRALRLLEPQIQLIRAI 216
DB 245 LSSKKKKFRRGPLNADLAILPYVYITFLESNKSVALQFQVRRVVOIFRIMRLIRL 304
OY 217 KTSNVSFKLSLSTLSTWFTAGFIHLVENSQDPWLK-----GRNSQINISYFESI 267
DB 305 KLANHSTGLSLGFTLRVSNELGLLFLAMGIMFSLVFAEKEDDTKFKSIFASF 364
OY 268 YLVWATTSYVGFQDVAKTSIGRTFIMFTLGLILFANYPVEVELFA-----NKRK 320
DB 365 WMAATITMTVGYGDIYDKPLTKIVGGLCCAGVIALPIPIVNNSEFYKQKROEK 424
OY 321 YTSYELKGRKFIVCGN---ITVDSVTAFLR-----NFLRDSKE 359
DB 425 AIKRREALERAK-----RNGSIYSNMKDAFARSIEMMDIYVERNGE 466

RESULT 5
CIRB_RAT STANDARD; PRT; 802 AA.
AC 063099;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV2.2 (CDRK).
GN KCM2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
ON NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MDLINE=92198655; PubMed=1550672;
RA Hwang P.M., Glatz C.E., Bret D.S., Yellen G., Snyder S.H.;
RT "A novel K+ channel with unique localizations in mammalian brain:
RT molecular cloning and characterization.";
RL Neuron 8:473-481(1992).
CC -|- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
CC CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
CC GRADIENT.
CC -|- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -|- TISSUE SPECIFICITY: IN THE BRAIN, THE GREATEST DENSITY OCCURS IN
CC THE OLFACTORY BULB, FOLLOWED BY THE CEREBRAL CORTEX, HIPPOCAMPUS,
CC AND CEREBELLUM. IN PERIPHERAL TISSUES IT IS MOST PROMINENT IN
CC WHOLE TONGUE EPITHELIUM AND CIRCUMVALLATE PAPILLAE.
CC -|- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION.
CC -|- DOMAIN: THIS TAIL MAY BE IMPORTANT IN MODULATION OF CHANNEL
CC ACTIVITY AND/OR TARGETING OF THE CHANNEL TO SPECIFIC SUBCELLULAR
CC COMPARTMENTS.
CC -|- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER
CC CLASS. BELONGS TO SHAB POTASSIUM CHANNEL SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M77482; AAA40905.1;
CC DR InterPro: IPR000636;

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DR InterPro: IPR003091;
DR Pfam: PF00520; Ion_trans. 1.
DR PRINTS: PR00169; KCHANNEL.
KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW Glycoprotein; Multigene family; Phosphorylation.
FT DOMAIN 1 190
FT TRANSMEM 191 212
FT DOMAIN 213 232
FT TRANSMEM 233 254
FT DOMAIN 255 264
FT TRANSMEM 265 286
FT DOMAIN 287 298
FT TRANSMEM 299 320
FT DOMAIN 321 334
FT TRANSMEM 335 356
FT DOMAIN 357 396
FT TRANSMEM 397 418
FT DOMAIN 419 802
FT DOMAIN 528 531
FT CARBOHYD 287 287
FT SEQUENCE 802 AA; 90702 MW; 792CC09A5DB28D7F CRC64;

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Query Match 2.88; Score 158; DB 1; Length 802;

Best Local Similarity 23.78; Pred. No. 0.0074;

Matches 60; Conservative 55; Mismatches 114; Indels 24; Gaps 6;

```

OY 103 QVLIVLVLVLSIGSLIYFINSADPVGSCSYEDKTIPDLVFNAFESFYEGLR 156
DB 193 KILAIIVLSLFTLSTALSLNTLPELOENDEFQPSD-NKRKLAIVEAVCIAMFMEYLRL 251
OY 157 FMAADKIKFMLEMNSIYDIFIPPTFISYLL-KSNMGLRFLRALRLLEPQIQLIRA 215
DB 252 FLSSPKMKFRRGPLNADLAILPYVYITFLESNKSVALQFQVRRVVOIFRIMRLIRI 311
OY 216 KTSNVSFKLSLSTLSTWFTAGFIHLVENSQDPWLK-----GRNSQINISYFESI 267
DB 312 KLANHSTGLSLGFTLRVSNELGLLFLAMGIMFSLVFAEKEDDTKFKSIFASF 371
OY 268 YLVWATTSYVGFQDVAKTSIGRTFIMFTLGLILFANYPVEVELFA-----NKRK 319
DB 372 FMAATITMTVGYGDIYDKPLTKIVGGLCCAGVIALPIPIVNNSEFYKQKROE 431
OY 320 KYTSYELKGRKFIVCGN 332
DB 432 KAIKRREALERAK 444

RESULT 6
CIRB_DROME STANDARD; PRT; 924 AA.
AC P17970;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN SHAB (SHAB11).
GN SHAB OR SHAB11.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Ephydroidea; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MDLINE=90239553; PubMed=2333511;
RA Wei A., Covarrubias M., Butler A., Baker K., Pak M., Salkoff L.;
RT "K+ current diversity is produced by an extended gene family
RT conserved in Drosophila and mouse.";
RL Science. 248:599-603(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MDLINE=90245668; PubMed=2336395;
RA Wei A., Covarrubias M., Butler A., Baker K., Pak M., Salkoff L.;

```

"Shal", Shab, and Shaw: three genes encoding potassium channels in Drosophila."

CC Nucleic Acids Res. 18:2173-2174(1990).

CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL GRADIENT.

CC -1- SUBUNIT: HETEROETRAMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).

CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

CC -1- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL TO SPECIFIC SUBCELLULAR COMPARTMENTS.

CC -1- MISCELLANEOUS: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.

CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER CLASS. BELONGS TO SHAB POTASSIUM CHANNEL SUBFAMILY.

CC -----

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CC -----

DR EMBL; M32659; AAA28896.1; -.

DR PIR; S15058; S15058.

DR HSSP; P01551; IACX.

DR FLYBase; FBgn0003383; Shab.

DR InterPro; IPR000636; -.

DR InterPro; IPR003091; -.

DR Pfam; PF00520; Ion_Trans. 1.

DR PRINTS; PR00169; KCHANNEL.

DR KVM; P00169; KCHANNEL.

KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel; Glycoprotein; Multigene family; Phosphorylation.

FT TRANSMEM 436 454 SEGMENT S1.

FT TRANSMEM 474 495 SEGMENT S2.

FT TRANSMEM 506 527 SEGMENT S3.

FT TRANSMEM 536 561 SEGMENT S4.

FT TRANSMEM 577 598 SEGMENT S5.

FT TRANSMEM 638 659 SEGMENT S6.

FT CARBOHYD 245 245 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 429 429 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 530 530 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 749 749 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 756 756 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 885 885 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 888 888 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT MOD_RES 690 690 PHOSPHORYLATION (BY CAPK) (POTENTIAL).

FT MOD_RES 731 731 PHOSPHORYLATION (BY CAPK) (POTENTIAL).

FT MOD_RES 796 796 PHOSPHORYLATION (BY CAPK) (POTENTIAL).

SO SEQUENCE 924 AA; 99698 MW; F4F74205C7020758 CRC64;

Query Match 2.7%; Score 157; DB 1; Length 924;

Best Local Similarity 23.1%; Pred. No. 0.011;

Matches 75; Conservative 69; Mismatches 125; Indels 56; Gaps 11;

DB 84 OGOFDHDH---LEMLAQOT-FVGQVIVLVFVLSGLIIFINSADPVGSCSSVEDKT 138

DB 411 EKEFSEIQKYLWELLEKPTSTFAARIATVISTLFVLSIALTLNLTLPOLQIIDGTPOD 470

DB 139 ID-----IDLVFNAPFFSYFGFLRFMAADDKIKFMLENSIVDITFIPPTGIS-YLIKSMNL 193

DB 471 NQGLAMVEAVCTWFTLETLIRFSSPKMKFFKGLNIIDILALIPYVSLFLETTNNK 530

DB 194 GL-RELRALRLLELPOLLIQILRAIKTS-----NSVFKSLKSLITLS---T 234

DB 531 ATDQDQVRRVVOVFIRMIKILVTLKLRHSTGLQSLGFTLRNSYKELGLMLFLAMGVLI 590

CC "Shal", Shab, and Shaw: three genes encoding potassium channels in Drosophila."

CC Nucleic Acids Res. 18:2173-2174(1990).

CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL GRADIENT.

CC -1- SUBUNIT: HETEROETRAMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).

CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

CC -1- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL TO SPECIFIC SUBCELLULAR COMPARTMENTS.

CC -1- MISCELLANEOUS: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.

CC -1- DOMAIN: THE TAIL MAY BE IMPORTANT IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL TO SPECIFIC SUBCELLULAR COMPARTMENTS.

CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER CLASS. BELONGS TO SHAB POTASSIUM CHANNEL SUBFAMILY.

CC -----

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CC -----

DR EMBL; U69962; AAB08433.1; -.

DR InterPro; IPR000636; -.

DR InterPro; IPR003091; -.

DR Pfam; PF00520; Ion_Trans. 1.

DR PRINTS; PR00169; KCHANNEL.

KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel; Glycoprotein; Multigene family; Phosphorylation.

FT TRANSMEM 191 190 SEGMENT S1 (POTENTIAL).

FT TRANSMEM 213 212 SEGMENT S1 (POTENTIAL).

FT TRANSMEM 233 232 SEGMENT S2 (POTENTIAL).

FT TRANSMEM 255 254 SEGMENT S2 (POTENTIAL).

FT TRANSMEM 265 264 SEGMENT S3 (POTENTIAL).

FT TRANSMEM 287 298 SEGMENT S3 (POTENTIAL).

SO DOMAIN

RESULT 7

CIRB_HUMAN STANDARD; PRT; 806 AA.

AC 092953;

DT 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 01-OCT-2000 (Rel. 40, Last annotation update)

DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV2.2.

GN KCNB2.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;

RM [1]

RP SEQUENCE FROM N.A.

RX MEDLINE;98275219; PubMed=9612272;

RA Schmalz F., Kinsella J., Koh S.D., Vogalis F., Schneider A., Flynn E.R., Kenyon J.L., Horowitz B.;

RT "Molecular identification of a component of delayed rectifier current in gastrointestinal smooth muscles."

RL Am. J. Physiol. 274:G901-G911(1998).

CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL GRADIENT.

CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.

CC -1- DOMAIN: THE TAIL MAY BE IMPORTANT IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL TO SPECIFIC SUBCELLULAR COMPARTMENTS.

CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER CLASS. BELONGS TO SHAB POTASSIUM CHANNEL SUBFAMILY.

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CC -----

DR EMBL; U69962; AAB08433.1; -.

DR InterPro; IPR000636; -.

DR InterPro; IPR003091; -.

DR Pfam; PF00520; Ion_Trans. 1.

DR PRINTS; PR00169; KCHANNEL.

KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel; Glycoprotein; Multigene family; Phosphorylation.

FT TRANSMEM 191 190 SEGMENT S1 (POTENTIAL).

FT TRANSMEM 213 212 SEGMENT S1 (POTENTIAL).

FT TRANSMEM 233 232 SEGMENT S2 (POTENTIAL).

FT TRANSMEM 255 254 SEGMENT S2 (POTENTIAL).

FT TRANSMEM 265 264 SEGMENT S3 (POTENTIAL).

FT TRANSMEM 287 298 SEGMENT S3 (POTENTIAL).

SO DOMAIN

DB 235 MFTAGFIHLVENSQDPWLKGNNSQNSISFESIYLVMTSTVGRGVVAKTSIGRTFM 294

DB 591 FSSLLVFAEKDE-----KDTKFSVSPFAFWAGITVTVGDICPTALGKVIQT 641

DB 295 FETLGLSLIFANYPIDWELFA-----NKRKYSSYEALGKKFIYCCGNIYDSTYA 347

DB 642 VCCICGVLVLPPIIYNNNAEPFKNQMRREKALKREALDRAK-----RGSLVS 693

DB 348 FLNRFLRD---KSGEINTEYFLGE 369

DB 694 FHHMLKDAFAKSMOLIDIVDTGK 718

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FT TRANSMEM 299 320 SEGMENT S4 (POTENTIAL).
FT DOMAIN 321 334 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 335 356 SEGMENT S5 (POTENTIAL).
FT DOMAIN 357 396 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 397 418 SEGMENT S6 (POTENTIAL).
FT DOMAIN 419 806 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 287 287 N-LINKED (GLCNAC. . .) (POTENTIAL).
SO SEQUENCE 806 AA; 90990 MM; 2AFBECBER05A90E6 CRC64;

Query Match 2.7%; Score 154.5; DB 1; Length 806;
Best Local Similarity 23.4%; pred. NO. 0.013;
Matches 58; Conservative 54; Mismatches 117; Indels 19; Gaps 5;

OY 104 VLVLIVFLVSLGSLIIVFINSADPVGSSSYED--KTIPIIDVFNAPSFYFGLRPMAD 161
DB 197 IVSILFIYLSTIALSLNLPIELQETDERGQLDNDRQLAHAVEVNCIAMPFTMEYLFRLSP 256
OY 162 DKIKEMLMNSIVDIPTIPPTFISYVL-KSNWGLRFLRALRLLELPQIILIRAKTSN 220
DB 257 NKKMKFFKPLNVIDLALPIVYVTFLEFNSKNSVLOFQVRRVQVIFRIMRILRIKLAR 316
OY 221 SVKFEKLSIILSTFTAGFIHLVENSQDPRLK-----GRNSQNIISYFEST----YLVM 271
DB 317 HSTGLQSLGFTLRNSYNELGLLLEFLAMGIMIESSLVFPAEKDEQATKPTIPASFWMAT 376
OY 272 ATTSTGFGDVYAKTSLGRPTFMFTFLGSLILFANYIPENWELFA-----NKRKYTS 324
DB 377 ITMTVGVGDIPKTLKIKYVGLCICAGVLIALPIPIVNNSEFYEKQKROKEAIR 436
OY 325 YEALGKR 332
DB 437 REALERAK 444

RESULT 8
CIRK2_HUMAN STANDARD: PRT; 499 AA.
AC P16389;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KVL1.2 (RBR2) (HBR5) (NGK1)
DE (NMK2) (HUKIV).
GN KCNA2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_Taxid:9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Brain;
RA Ramayam M., Gautam M., Kamb A., Rudy B., Tanouye M.A.,
RA Mathew M.K.;
RT "Human potassium channel genes: molecular cloning and functional
RT expression.";
RL Mol. Cell. Neurosci. 1:214-223(1990).
CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
CC CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
CC GRADIENT.
CC -1- SUBUNIT: HETEROTETRAMER OF POTASSIUM CHANNEL PROTEINS (PROBABLE).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- DOMAIN: THE AMINO TERMINUS MAY BE IMPORTANT IN DETERMINING THE
CC RATE OF INACTIVATION OF THE CHANNEL WHILE THE TAIL MAY PLAY A ROLE
CC IN MODULATION OF CHANNEL ACTIVITY AND/OR TARGETING OF THE CHANNEL
CC TO SPECIFIC SUBCELLULAR COMPARTMENTS.
CC -1- DOMAIN: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND IS
CC CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
CC EVERY THIRD POSITION.
CC -1- SIMILARITY: THIS CHANNEL PROTEIN BELONGS TO THE DELAYED RECTIFIER

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CC      CLASS: BELONGS TO SHAKER POTASSIUM CHANNEL SUBFAMILY.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@sib-sib.ch).
CC      -----
DR      EMBL; L02752; AAA36141.1; -.
DR      HSSP; P03621; 21FN.
DR      MIM; 176262; -.
DR      InterPro; IPR000636; -.
DR      InterPro; IPR030391; -.
DR      Pfam; PF00520; Ion_trans; 1.
DR      PRINTS; PR00169; KCANNEL.
KW      Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;
KW      Glycoprotein; Multigene family; Phosphorylation.
FT      TRANSMEM 164 182 SEGMENT S1.
FT      TRANSMEM 222 243 SEGMENT S2.
FT      TRANSMEM 255 275 SEGMENT S3.
FT      TRANSMEM 293 311 SEGMENT S4.
FT      TRANSMEM 328 347 SEGMENT S5.
FT      TRANSMEM 389 411 SEGMENT S6.
FT      CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD 207 207 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      MOD_RES 449 449 PHOSPHORYLATION (BY CAPK) (POTENTIAL).
SQ      SEQUENCE 499 AA; 56716 MM; 4B03F1B46A826C39 CAC64;
      Query Match 2.6%; Score 147; DB 1; Length 499;
      Best Local Similarity 22.3%; Pred. No. 0.02;
      Matches 77; Conservative 64; Mismatches 132; Indels 72; Gaps 13;
QY      104 VLVIIVLPVLSI-----GSLIIFPNSADPVG--SCSYEDKTIPIDLVF 145
DB      170 VMLVILISVSCLETLPPIFDENEDMHSGVFHYTSSITGVOQSTFDPFIETVLC 229
QY      146 NAFEEFYGLFPMADDKIKFWLEKNSIVDFTPTPTISYLK-----SNMLG 194
DB      230 IIMSFEEFLVYFNFACPSKAGFFTNIMNIIDVAILPIPTLTGLTELAKPEDAQOQOAMS 289
QY      195 LRFPLRLLELPQI-----LQII-RAIKTS-----NSYKESKLLSIILSTWFTAG 240
DB      290 LAIRKIVILAVYEVRFIKLSRHSKGLQIIIGQTLKAMREIGLIFLFGVIL--FSSAV 346
QY      241 FHLVENSQDPMKGRNCONISYFESIYLVMAVTSVGEQDVAVTSGRTPIMFETLGS 300
DB      347 YFAEAD-----REQQPSIPAFMVAAYSMITVGVGDWVPITIGKIVGSLCAIAG 398
QY      301 LILFANYIPEWVELFANKRKYTSYEALKGKFIYV--CGNI-----IVDSYTAFLR 350
DB      399 VLTIALPVPVIVSNF--NYFYHRETEGEEOAOYLQVTSCKPIPSSPDLKKSRSATSKS 456
QY      351 NPLRDKGEINTEIYELGETPPSLELETIFPCYLAATYFISGSAM 395
DB      457 DIMELQEGVNNNSNEDFREE-----NLKTA-NCTLANTNYVNIITKM 495
CC      RESULT 9
CC      CIRK2_MOUSE STANDARD; PRT; 499 AA.
AC      01-APR-1990 (Rel. 14, Created)
DT      01-AUG-1990 (Rel. 15, Last sequence update)
DT      15-JUL-1998 (Rel. 36, Last annotation update)
DE      VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KVL1.2 (RBK2) (RCK5) (NGK1)
DE      (NMK2) (HUKIV).
GN      KCNA2.
OS      Mus musculus (Mouse), and Rattus norvegicus (Rat).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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Db 258 DEVEDIELRKFKVIEKDESLAY--KSLKDNIRKGTATIGIRREKFCINPYPE 311

RESULT 12

C101_HUMAN STANDARD; PRT; 676 AA.

AC P51787; Q92960; O00347; O60607;

DT 01-OCT-1996 (Rel. 34, Created)

DT 15-JUL-1998 (Rel. 36, last annotation update)

DT 01-OCT-2000 (Rel. 40, last annotation update)

DE VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KQT-LIKE 1 (KVL 9).

GN KCONQ1 OR KCNA9 OR KVLQ1 OR KCNA8.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_Taxid=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Kidney;

RX MEDLINE-9745933; Pubmed-9312006;

RA Chouabe C., Neyroud N., Guicheney P., Lazdunski M., Romey G.,

RT "Properties of KVLQ1 K+ channel mutations in Romano-Ward and Jervell

RT and Lange-Nielsen inherited cardiac arrhythmias.";

RL EMO J. 16:5472-5479(1997).

RN [2]

RP SEQUENCE OF 96-156 FROM N.A.

RC TISSUE=Pancreas;

RX MEDLINE-9705936; Pubmed-8900283;

RA Sanguinetti M.C., Curran M.E., Zou A., Shen J., Spector P.S.,

RT "Coassembly of K(V)LQ1 and minK (Isk) proteins to form cardiac I(Ks)

RT potassium channel.";

RL Nature 384:80-83(1996).

RN [3]

RP SEQUENCE OF 1-129 FROM N.A.

RX MEDLINE-9726869; Pubmed-9108097;

RA Yang W.P., Levesque P.C., Little W.A., Conder M.L., Shalaby F.Y.,

RT "KVLQ1, a voltage-gated potassium channel responsible for human

RT cardiac arrhythmias.";

RL Proc. Natl. Acad. Sci. U.S.A. 94:4017-4021(1997).

RN [4]

RP SEQUENCE OF 130-676 FROM N.A., AND VARIANTS LQ1.

RX MEDLINE-9612203; Pubmed-8528244;

RA Wang Q., Curran M.E., Splawski I., Burn T.C., Millholland J.M.,

RA Varrault J., Shen J., Timothy K.W., Vincent G.M., de Jager T.,

RA Schwartz P.J., Towbin J.A., Moss A.J., Atkinson D.L., Landes G.M.,

RT "Positional cloning of a novel potassium channel gene: KVLQ1

RT mutations cause cardiac arrhythmias.";

RL Nat. Genet. 12:17-23(1996).

RN [5]

RP SEQUENCE FROM N.A. (ISOFORM TKVLO1).

RC TISSUE=Heart;

RX MEDLINE-97450920; Pubmed-9305853;

RA Jiang M., Tseng-Crank J., Tseng G.-N.;

RT "Suppression of slow delayed rectifier current by a truncated isoform

RT of KVLQ1 cloned from normal human heart.";

RL J. Biol. Chem. 272:24109-24112(1997).

RN [6]

RP VARIANTS LQ1 SER-314 AND VAL-341.

RX MEDLINE-97026293; Pubmed-8872472;

RA Russell M.W., Dick M. II, Collins F.S., Brody L.C.;

RT "KVLQ1 mutations in three families with familial or sporadic long QT

RT syndrome.";

RL Hum. Mol. Genet. 5:1319-1324(1996).

RN [7]

RP VARIANTS LQ1 PRO-178; MET-313; ARG-325 AND PRO-366.

RT "Four novel KVLQ1 and four novel HERG mutations in familial long-QT

RT syndrome.";

RL Circulation 95:565-567(1997).

RN [8]

RP VARIANTS LQ1.

RX MEDLINE-98045903; Pubmed-9386136;

RA Donger C., Denjoy I., Berthet M., Neyroud N., Cruaud C., Benaecour M.,

RA Chivoret G., Schwartz K., Coumel P., Guicheney P.;

RT "KVLQ1 C-terminal missense mutation causes a forme fruste long-QT

RT syndrome.";

RL Circulation 96:2778-2781(1997).

RN [9]

RP VARIANTS LQ1 ARG-216.

RX MEDLINE-97418118; Pubmed-9272155;

RA van den Berg M.H., Wilde A.A.M., Robles de Medina E.O., Meyer H.,

RA Geelen J.L.M.C., Jongbloed R.J.E., Wellens H.J., Geraedts J.P.M.;

RT "The long QT syndrome: a novel missense mutation in the S6 region of

RT the KVLQ1 gene.";

RL Hum. Genet. 100:356-361(1997).

RN [10]

RP VARIANTS LQ1 ASN-317.

RX MEDLINE-98027069; Pubmed-9302275;

RA Wolinik B., Schroeder B.C., Kubisch C., Esperer H.D., Wleackner P.,

RA Jentsch T.J.;

RT "Pathophysiological mechanisms of dominant and recessive KVLQ1 K+

RT channel mutations found in inherited cardiac arrhythmias.";

RL Hum. Mol. Genet. 6:1943-1949(1997).

RN [11]

RP VARIANTS LQ1 VAL-341.

RX MEDLINE-98230121; Pubmed-9570196;

RA Li H., Chen Q., Moss A.J., Robinson J., Goytia V., Perry J.C.,

RA Vincent G.M., Priori S.G., Lehmann M.H., Denfield S.W., Duff D.,

RT "New mutations in the KVLQ1 potassium channel that cause long-QT

RT syndrome.";

RL Circulation 97:1264-1269(1998).

RN [12]

RP VARIANTS LQ1 THR-300.

RX MEDLINE-98303396; Pubmed-9641694;

RA Priori S.G., Schwartz P.J., Napolitano C., Bianchi L., Dennis A.,

RT "A recessive variant of the Romano-Ward long-QT syndrome?";

RL Circulation 97:2420-2425(1998).

RN [13]

RP VARIANTS LQ1 SER-305.

RX MEDLINE-98434341; Pubmed-9781056;

RA Neyroud N., Denjoy I., Donger C., Gary F., Villain E., Leenhardt A.,

RA Bernal K., Schwartz K., Coumel P., Guicheney P.;

RT "Heterozygous mutation in the pore of potassium channel gene KVLQ1

RT causes an apparently normal phenotype in long QT syndrome.";

RL Eur. J. Hum. Genet. 6:129-133(1998).

RN [14]

RP VARIANTS LQ1 ARG-168; SER-314; CYS-315; ASN-318; PRO-353 & TRP-366.

RX MEDLINE-98360095; Pubmed-9693036;

RA Splawski I., Shen J., Timothy K.W., Vincent G.M., Lehmann M.H.,

RT "Genomic structure of three long QT syndrome genes: KVLQ1, HERG, and

RT KCNEL.";

RL Genomics 51:86-97(1998).

RN [15]

RP VARIANTS LQ1 ILE-312 AND ASN-317.

RX MEDLINE-98141684; Pubmed-9482580;

RA Saarinen K., Swan H., Kainulainen K., Tolonen L., Viitasalo M.,

RT "Molecular genetics of the long QT syndrome: two novel mutations of

RT the KVLQ1 gene and phenotypic expression of the mutant gene in a

RT large kindred.";

RL Hum. Mutat. 11:158-165(1998).

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OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxId=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88122563; PubMed=2448635;
 RA Schwarz T.L., Tempel B.L., Papazian D.M., Jan Y.N., Jan L.Y.;
 RT "Multiple potassium-channel components are produced by alternative
 RT splicing at the Shaker locus in Drosophila."
 RL Nature 331:137-142(1988).
 RN [2]
 RP SEQUENCE OF 1-349 FROM N.A.
 RC STRAIN=CANTON-S;
 RX MEDLINE=88396413; PubMed=2456921;
 RA Pongs O., Kerschmethyl N., Mueller R., Krah-Jentgens I., Baumann A.,
 RA Kiltz H.H., Canal I., Llamazares S., Ferrus A.;
 RT "Shaker encodes a family of putative potassium channel proteins in
 RT the nervous system of Drosophila."
 RL EMBO J. 7:1087-1096(1988).
 CC -1- FUNCTION: THIS PROTEIN MEDIATES THE VOLTAGE-DEPENDENT POTASSIUM
 CC ION PERMEABILITY OF EXCITABLE MEMBRANES. ASSUMING OPENED OR CLOSED
 CC CONFORMATIONS IN RESPONSE TO THE VOLTAGE DIFFERENCE ACROSS THE
 CC MEMBRANE, THE PROTEIN FORMS A POTASSIUM-SELECTIVE CHANNEL THROUGH
 CC WHICH K+ IONS MAY PASS IN ACCORDANCE WITH THEIR ELECTROCHEMICAL
 CC GRADIENT.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- ALTERNATIVE PRODUCTS: 4 ISOFORMS ARE PRODUCED BY ALTERNATIVE
 CC SPLICING.
 CC -1- MISCELLANEOUS: THE SEGMENT S4 IS PROBABLY THE VOLTAGE-SENSOR AND
 CC IS CHARACTERIZED BY A SERIES OF POSITIVELY CHARGED AMINO ACIDS AT
 CC EVERY THIRD POSITION.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: X07134; CAA30146.1; -
 CC EMBL: X06742; CAA29917.1; -
 CC PIR: S00482; S00482.
 CC PIR: S00508; S00508.
 CC FLYbase: FBgn0003380; Sh.
 CC InterPro: IPR000636; -
 CC InterPro: IPR003091; -
 CC Pfam: PF00520; Ion.trans.1.
 CC PRINTS: PR00169; KCHANNEL.
 CC DR Ion channel; Transmembrane; Ion transport; Voltage-gated channel;
 CC Glycoprotein; Alternative splicing; Multigene family.
 CC KW TRANSMEM 228 246
 CC FT TRANSMEM 279 300 SEGMENT S1.
 CC FT TRANSMEM 311 332 SEGMENT S2.
 CC FT TRANSMEM 358 382 SEGMENT S3.
 CC FT CARBOHYD 102 102 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 259 259 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 263 263 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 625 625 N-LINKED (GLCNAC. . .) (POTENTIAL).
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Query Match 2.4%; Score 139.5; DB 1; Length 656;
 Best Local Similarity 20.8%; Pred. No. 0.093;
 Matches 58; Conservative 55; Mismatches 109; Indels 57; Gaps 8;

OY 104 VLVILVFLVSLIGSLIYFINS-----DPVSCSSYEDKTI-----IDLVFN 146
 DB 229 VAIISVAVILLSIVIFCLFETLPEFKHYKVFNTTNGTKIEDEVDIDDPFLIETLCI 287
 OY 147 AEFSEYFGELRFMAADKIKFMLEMNSIVDIFITPTFISYLL----- 188
 DB 288 IMWTFELFLYRFLACPKLNCRDVMNVIDIALIIPYFITLATVVAEEDTLNPKAPVSP 347

OY 189 ----KSNWLGRLRLRLRLLELPOLLIILRAITSNVSKEFKLSITLSTWTTAG---- 240
 DB 348 QDKSSNQAMSLAILRYIRL-----VRVERIFKLSHSGKLIQLGRRLKASMRLEGLIF 401
 OY 241 --FIHLVENSQDPMWLGKRNQNSISYFESI-----YLVWATSTYVFGDVAKTSIGFTFM 294
 DB 402 FLFIGVALLSSAVYFADAGSEN-SFKRSIPDAFMAVVTWTTVGYGDMTPVGVWGAIVGS 460
 OY 295 FETIGSLILFANYIPEWVELFANKRKRYTSSYEALGKRF 333
 DB 461 LCAIAGVLTALPVPVIVSNFNYFHRETQDEMQSNF 499

Search completed: October 5, 2001, 12:12:26
 Job time: 568 sec

Db 361 NIIIVLGELEPCLEETLTKCHTSCNFCVGTALKEFDKRAVENSEACLIILANFCS 420
421 DSAEDISNIMRYLSTIKNDSTRTIIOILOSNNKYLPKIPSMNDGTNIICFAELKL 480
Db 421 DLHEDNSNIMRYLSTIKNYPOTRVIIOILOSNNKYLPKIPSMNDGTNIICFAELKL 480
481 GFLAOGCLVPGCLFTLSLFEVONKVMKPKOTWKHFNLMSKNNKILTORLSDDFAGMSFP 540
Db 481 GFLAOGCLVPGCLFTLSLFEVONKVMKPKOTWKHFNLMSKNNKILTORLSDDFAGMSFP 540
541 EVARLCEFLAKYLLILAEKSLFTDGCGLILPPPOVRIKNTLGEFLIETPKDYRAL 600
Db 541 QVSRLECFVKLMILAIQHPFE-HSCCTILIMPSSOVRLNKDITLGEFLIDSSKAKYRAF 599
601 FYCSVCHDVPFIPELITNCGCKSRHOHITVPSVKRMKCKLKGISRSISGODSPRVSAS 660
Db 600 FYCSNCHSDVCPNELIGCKCKIKSRQOLAPTIMYKSSLTDPFTT-SSHINAMS 654
661 T-----SSISNFTTRLOHVDIEDSDOLDSSGMFMCKPTSLDKVTLKRTGSK 709
Db 655 TEIHGFSRPOSLITITNRPPTNDVTDOTMLDSSGMFMCKRAMPLDKVTLKRSKAK 714
710 YKRNITVACVGDASAPRGLNFMPLRASNYTRKELDIYFISLDYLOREMPRLN 769
Db 715 HEONHIVVCVGDACCTGLNFMPLRASNYTRKELDIYFISLDYLOREMPRLN 774
770 FPOIYILPCALYSGDLHAANIEGSCMCAVLSPPPOSSNOTLVDTREALMATLISLOI 829
Db 775 FPHIHMPGALYMGDLIAVNEGSCMCAVLSPPPOSSNOTLVDTREALMATLISLOI 834
830 DSSSDPSVSEETPGYT-NGHNEKSNCRKVPILTELKNSNHFIEQLGSLQETN 888
Db 835 -TSPTGSSSSEKVPSSAFSKERKORQIPILTELKNSNHFIEQMLGMLKGT 893
889 LHTSTFSGTGVSSSFLDSLATAFYNVHVELLMYTGVSQLEOHLDKXYGVA 948
Db 894 LHTSTFSGTGVSSSFLDSLATAFYNVHVELLMYTGVSQLEOHLDKXYGVA 953
949 DCSSTLSGHRNCKGLLSHETILSDVNPFRNFGOLFCSGLDILGILCYGLRIIDEE 1008
Db 954 DDEAIKSGTRCKLGLSLDQVLSGINRKRFGOLFCSGLDILGILCYGLRIIDEE 1013
Qy 1009 LNPENKRPVITRANEFKLLPSDLVCAIPFSTACYK 1045
Db 1014 PEOENKRPVITRANEFKLLPSDLVCAIPFSTACYK 1050
RESULT 2
S62904
calcium-regulated potassium channel alpha chain - human
C:Species: Homo sapiens (man)
C:Date: 24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
C:Accession: S62904
R:Meera, P.; Wallner, M.; Jiang, Z.; Toro, L.
FEBS Lett. 382, 84-88, 1996
A:Title: A calcium switch for the functional coupling between alpha (hslc) and beta subunit (hslb) of the calcium channel alpha1G1
A:Reference number: S62904; M01D:96196569
A:Accession: S62904
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-1113 <ME>
A:Cross-references: EMBL:011058; NID:g507921; PID:g507922
A:Note: the nucleotide sequence was submitted to the EMBL data library, June 1994

Query Match 41.2%; Score 2355.5; DB 2; Length 1113;
Best Local Similarity 43.4%; Pred. No. 2.8e-157;
Matches 482; Conservative 196; Mismatches 328; Indels 105; Gaps 17;
Qy 26 AFLISFVTFPSGLILFRLIMRSVK-KM-----OIKGTGILLETFS 70
Db 24 AFLASSMVFPGGLFI-----LAKRIKLYIMTYCCHGCKTKRAQKINSS-----QAD 74

Qy 71 GTI-----ARSHVRSLEHFOGRDHIEMLSAQTEGOVILVILVLSIGSLIYFNS 124
Db 75 GTLKPVDKEEAAAEVGMWTSVKDAGVIMASQITLGRVLVLRVLSLALVITYFIDS 134
Qy 125 ADPVGSCSS-YEDKTIPIIDVFNAPFSYFGRLRPMADDKIKFLEWNSIVDIPTPTF 183
Db 135 SNPIESQNFYKFFTLQIDMAFNVFFLLYGLRFLIANDKMLEVNSVYDEFTVPVF 194
Qy 184 ISYILKSNMGLRFLARLLELPOLILRAIKTSNVSFSLSLISTLSTWTAAGFIH 243
Db 195 VSVYLNRSWGLRFLARLLELPOLILRAIKTSNVSFSLSLISTLSTWTAAGFIH 254
Qy 244 LVNSGDPMLKGRNNSNISYFESILYVMATTSYVGEDVAKSLSGTFIMFTLSLIL 303
Db 255 LVNSGDPMPNPNONALTYVECVLLMYTMSYVGQDYAKTTLGRLEVFETLGLAM 314
Qy 304 FANYIPMVELFANKRKYTSYSEALGKKFTIVCGNITVDSVTAFLRNLDRKSGEINTE 363
Db 315 FASYVEIIEILIGNRRKYGGSYAGVRKHIVVCGHITLESVNFLLKDFLHKRDQVNE 374
Qy 364 IYFLGTPSLELETFKCYLATTTTSSGAMKEEDLRVAVSAREACLIILANPLCSDSH 423
Db 375 IYFLHNSPYLELEALFKRFTQVEFYQGSVLNPHDLARVAKIESADCLILANKCADPD 434
Qy 424 AEDISNIMRYLSTIKNDSTRTIIOILOSNNKYLPKIPSMNDGTNIICFAELKLGT 483
Db 435 AEDASNIMRYLSTIKNHPKRIITOMIYNKKAHLINIPSMNKEBDGALCLAEKLGT 494
Qy 484 AOGCLVPGCLFTLSLFEVONKVMKPKOTWKHFNLMSKNNKILTORLSDDFAGMSPEVA 543
Db 495 AOGCLVPGCLFTLSLFEVONKVMKPKOTWKHFNLMSKNNKILTORLSDDFAGMSPEVA 554
544 RLCEFLMYLLILAEKSLFTDGCGLILPPPOVRIKNTLGEFLIETPKDYRALFYC 603
Qy 555 ELCEFLMYLLILAEKSLFTDGCGLILPPPOVRIKNTLGEFLIETPKDYRALFYC 612
Db 555 ELCEFLMYLLILAEKSLFTDGCGLILPPPOVRIKNTLGEFLIETPKDYRALFYC 612
604 SYCHDVPFIPELITNCGCKSRHOHITVPSVKRMKCKLKGISRSISGODSPRVSASTSS 663
Db 613 KACHDITDPRKIRKCGCK--RLEDEOPSTLSPK--KQKNGCMRNSP----- 656
Qy 664 ISNFTTRLOH-----VEGDSQOLDSSGMFMCKPTSLDKVTLKRTGSKYK 711
Db 657 -NTSPRLMHRDULLIPGNDQIDNMDSNVKRYDSTGFHCAKREIEKYLTLTSEAMTV 714
712 FRNHIYACVGDASAPRGLNFMPLRASNYTRKELDIYFISLDYLOREMPRLNFP 771
Db 715 LSGHVYVCIFGDVSSALIGRLNFMPLRASNYTRKELDIYFISLDYLOREMPRLNFP 774
Qy 772 QIYILPCALYSGDLHAANIEGSCMCAVLSPPPOSSNOTLVDTREALMATLISLOI 830
Db 775 KVSILPQTPSLRADLRAVINILCDMCKVIISANONNIDTSLQDEKICILASLNKSMQFD 834
Qy 831 -----SSSDPSVSE-ETPGYTNGHNEKSNCRKVPILTELKNSN 870
Db 835 SICIVLOANSOGTTPCGMDKSSPDNSPVHGMRLKROPSTTGVN-----PITTELVDNTN 887
Qy 871 IHPIEDLGLESLQETNHLSTAFSTGTVFSSSFLDSLATAFYNVHVELLMYTGVS 930
Db 888 VQFLDQ---DDDDDPTELYLTPFACGTAFAYVDSLSMSATYFNDILTLRLTVGS 944
Qy 931 VSSQLDQHDKQYVYVADSCVLSGHRNCKGLLSHETILSDVNPFRNFGOLFCSGL 990
Db 945 ATPELBALIAEENALRGYSTPQTLANRDRCAVOALALLDGPADLGDGCYDCLCKAL 1004
Qy 991 DLFGIICVGLYRIIDEEELNPE--NKRFPVITRANEFKLLPSDLVCAIPFSTACYK 1048
Db 1005 KTYNMLCFGYLRDLNHLSTPQCTKRYVTNPPYFELVPTDLIFCLAQF----- 1055
Qy 1049 EFLSLQSYEIVNKAQSTEDTFRHKLSHPL 1079
Db 1056 DHNAGOSRASLSHSHSSQSSSKSSSVSHI 1086


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Db 392 TLETSVNFKDFLHKDRDVNVEIVLHNI SPNLELEALFKRHFTOVEFGQSVLPNHD 451
Oy 401 RRAVASEACILIANPLCSDHAEDISINIMRVLSIKNTDSTRIITIOLOSHNKYLPR 460
Db 452 ARKATISADACILANKYCADPDAEASINIMRYISIKNHPKRIITOMLOYNKHAHLN 511
Oy 461 IPSMNDTGNIIICFAELKLGFAOGLVPGCTFTLSFEVQNKVMPKQTKHFLNS 520
Db 512 IPSMNRKEGDDAICLAELKLGFAOGLVPGCTFTLSFEVQNKVMPKQTKHFLNS 571
Oy 521 MNKILITOLSDDFAGMSRPEVARLCFLMAYLLILAIKESLFTDQFC--GLILNPPQY 578
Db 572 VSNEMTEFLSSAFGLSPPTCELCFKLMLAIEXKSNANRESRKRRIINPGNHL 631
Oy 579 RIRKNTLGRFIAETPKDVRRLAFECVCHDDVEIPPELLNCGCKSRROHITVPSYRKM 638
Db 632 KIOEGLGFLFMSDAKEVARAFYCKACHDDYTDPRKIKKCGC--RLDEQCPITLSPKK 669
Oy 639 KCLKGISSRISGQDSPRVASASTSISNFTTQLQHD-----VEQSDQLDSS 686
Db 690 K-----QHNCGMRNSP-----NTSPKLMRHPDLPILPGNDQIDNMDSNVKKYDST 733
Oy 687 GNFHCKPPTSLDKVTLKRTGSKYKFRNHIIVACVFGDAHSAPGLNFMPLRASKYTRK 746
Db 734 GNFHCKAPETIEKVLITRSEAAATVLSGHVVCIFEDVSSALGLNLVPLASNFHYH 793
Oy 747 ELKDIVETSLDYLOREMFELRNFOIYILPGCALYSGDLHANIEQCSMCALVSPPOP 806
Db 794 ELKHIYFVGSIEYELKREWEFTLNHPKVSILPGTPSLRADLRANINIMCMCVILSNQNN 853
Oy 807 SSNOILVDTALMATITTSLOID-----SSDPSPVSE--ETPG 845
Db 854 IDDTSLQDEKICILASLNKSKQFDSIGVLOANSOGFTPPGMDRSSPDSNPGMLRQPS 913
Oy 846 YTNCHN-----EKSNCRKVPILTELKNSNHFIEOLGLEGSLQ 885
Db 914 ITTGVAIPITTELARKGKPLVSVNDEKNSGTHIIMTELVDNTOQFDO--DDDDP 970
Oy 886 ETNLHLSTAFTGTVFSSFLDLSLATAFYNYHVELLOMLTVGVSQLEOHLDKYV 945
Db 971 DRELVTLOPFACGTAFVAVSVLDSMSATYFNDNIILFLITVYTGATPELEALIAENML 1030
Oy 946 GVADECTSLLSRNCKGLLSLHETILSDVNPRTFGQLFCGSLDFGLCYGLYRIID 1005
Db 1031 RCGYSTPQTLARNDCRVAQLALLDGPFPADLDGCGYDLFCALTYNMLCFGIRLND 1090
Oy 1006 EBEELNPE--NKRFPVITRPANEFKLPSPDVFCAIPFSTACYKRNEEFSLOKSEIYNKAS 1063
Db 1091 AHLSTPSQCTKRYVITNPRYEFELVPTDLIFCLMQF-----DHNAQSRASLSHS 1141
Oy 1064 OTTETDFRHKLSHPL 1079
Db 1142 HSSQSSSKSSSVHSI 1157

RESULT 5
JH0697
C:Species: Drosophila melanogaster
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #texl_change 24-Sep-1998
C:Accession: JH0697
R:Adelman, J.P.; Shen, K.Z.; Kavanaugh, M.P.; Warren, R.A.; Wu, Y.N.; Lagrutta, A.; Bond
Neuron 9, 209-216, 1992
A:Title: Calcium-activated potassium channels expressed from cloned complementary DNAs.
A:Reference number: JH0697; MUID:92360298
A:Accession: JH0697
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-1175 <ADE>
A:Cross-references: GB:M96840; NID:9157775; PID:9157776
C:Comment: This potassium channel protein is activated by calcium.
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A:Gene: FlyBase:slo
A:Cross-references: FlyBase:FBgn0003429
C:Keywords: alternative splicing; calcium binding; ion channel; potassium channel; tr
F:126-143/Domain: transmembrane #status predicted <TM1>
F:165-186/Domain: transmembrane #status predicted <TM2>
F:196-214/Domain: transmembrane #status predicted <TM3>
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F:761-772/Domain: calcium binding #status predicted <CAL>

Query Match 35.0%; Score 2002.5; DB 2; Length 1175;
Best Local Similarity 38.7%; Pred. No. 2e-132;
Matches 434; Conservative 188; Mismatches 356; Indels 143; Gaps 17;

Oy 27 FILSSVTPFSGILITLIPLI-----RSYKMQIILKGTGILE 66
Db 52 FILSSVTFPLAGLVLLVLMNAFAFVCCCKREPDLPNDPKQEKASRNKQEFCT----- 106
Oy 67 LFTSGTARSVHSLHFGQFDRHIELLSAQTFVGOVILVFLVSLIGSLIYFTN-SA 125
Db 107 -----FMTEAKDMAGELISGOTTGRILVVLVFLISLISLIYFDASS 150
Oy 126 DPGSCSSYEDK-TIPIDLVNAPFSPYRGLRMAADDKTKFLEMNSIYDITPTPTI 184
Db 151 EEVERQOKSNNTQOIDLAFNIFEMVYFIRPIAASDKLMFLMWSFYVDYETIPSPFV 210
Oy 185 SYLKSNMLGRLRLRLLELPOLIOILRAIKTSNVKPSKLSLITLSTWTFPAAGFIHL 244
Db 211 SYLDWTGRLRLRLRLMTVPDIQYLVNLTSSSIRLAQVLSFISWLTAAGIHL 270
Oy 245 VENSQDPMWLGKRNISONISYFESTIYLVMTSTVGFQDVVAKTSLGRTFMFTLGLSLIF 304
Db 271 LENSQDP-LDFDNAHLRSLWTCVYFLITMSTVGYGDVCEYVGLFVFLVGLAMF 329
Oy 305 ANYPRMVELFANKRKYTSYELAKKKFTVNGCINTVDSVTFELNPLRDKGELINTEL 364
Db 330 ASSIPETIELVSGNKYGGELKREHGRHIVVCGHTYESVSHFLDFLEHREDVDVEV 389
Oy 365 VFLEGPSPLELETIFKCYLAATYFTISGSMKWEEDLRVAVASEACILIANPLCSDSNA 424
Db 390 VFLEHRPRDLEGLRKHFHTYVEFGQITMNPIDQKRVHADADCVLANKYCODPDA 449
Oy 425 EDISINRVLSIKNDSTRIITIOLOSHNKYVLPKIPSNMNDGNIICFAELKGFIA 484
Db 450 EDANIMIRVLSIKNSDDIRVLIQLOYNKAYLILIPSDMKQGDVLCIAELKGFIA 509
Oy 485 OGGLVPGCTFTLSFEVQNKVMP-KOTWKKHFLSMKMKILTORLSDDFAGMSRPEVA 543
Db 510 QSCLAGFSTMANLFRAMSFKTSPMQSWTNDYLRGCTGHEMTETLSLPTFGIIPRAQAT 569
Oy 544 RLCEFLMYLLLAIEYKSLFTDQFCGLINPPQVIRKNTLQFTLAETPKDVRRLAFYC 603
Db 570 ELCEFKILLLLAIEIKGA-EEGADSKISINPRGAIQANTQGFIAQSDAEVKRAMFVC 628
Oy 604 SYCHDVFTPELTNCGCK-----SRSQHITV----- 631
Db 629 KACHEDIKDETLKKCKKNLVQVPRSKFDDLDITRDREDTILNRNVRPRTGNGTG 688
Oy 632 -----PSYRKMCKLKGISRSISGO--DSPRVASASTSISNFTT-- 669
Db 689 GHHNMNTAAAAAAGAKQYKVKVPTV-IVSRQYEGOVISQVNRPTSRSSSGICTON 747
Oy 670 -----RTLQHDVEQSDQLDSSGNFHNCKPSTLDPKVTLKRTGSKYKFRNH 715
Db 748 QNGGVSLPAGIADQSKDPDFEKTEKKYDSTGFMHSPAKSLIEDCLDRNQAMVPLNCH 807
Oy 716 IVACVFGDAHSAPMGKLRNVPLRASNYTRKELDIVTIGSLDYLOREKRFELRNFOIYI 775
Db 808 VVVCLEFADDDSLIGLRNLVMPLRASNFHYHELKHIYVIGSVYDIRREKMKLQNLPIKISV 867
Oy 776 LPGCALYSGDLHAANIEQCSMCALVSPPOPSSNOILVDTALMATITTSLOID----- 830
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Db 868 LNSGSPSLRADLRVAVNNLCMCCILSAKPVNDPDLADKREAILASINIKAMPEDDTIGV 927
 QY 831 -----SSDPSVSEETPGYTNHNEKSNCRKVPILTELKNPSNIHFIEOLGG 879
 Db 928 LSGRPFEDLSKATAGSPIYQRR-GSYVGAN-----VPMITELVNDGNGVQFLDQ--- 976
 QY 880 LEGSLQETNLHLSTAFSTGTGVFSSSFLDSLATAFYVHYVHLELLQMLVTGVSQSLQHL 939
 Db 977 DDDDDPDTLEYLTQPFACGAFAYSVLDSLMSSTYFNQNLTLIRSLITGGAPELELIL 1036
 QY 940 DKDKYGVADVASCSTLSGGRKCKIGLSLHETILSDVNPFRNTQQLFCGSLDLFGIICVG 999
 Db 1037 AEGAGLNGSYSTVESLSNRRCRGOISLYDGLAOPGECGKYDDELVAALKSXYMLCIG 1096
 QY 1000 LYRLID-EELNPNKRFVITRPNNEFKLLPSDLVFCALPF 1039
 Db 1097 LYRFRDTSSSCDASSKRYITNPDPDSLPTDQVFLMQF 1137

RESULT 6

A39800
 Calcium-activated potassium channel, composite form - fruit fly (*Drosophila melanogaster*)
 C:Species: *Drosophila melanogaster*
 C:Date: 27-Mar-1992 #sequence_revision 27-Mar-1992 #text_change 01-Dec-2000
 C:Accession: A39800; PS0444
 R:Atkinson, N.S.; Robertson, G.A.; Ganetzky, B.
 Science 253, 551-555, 1991
 A:Title: A component of calcium-activated potassium channels encoded by the *Drosophila* s
 A:Reference number: A39800; MIMD:91313401
 A:Accession: A39800
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-1184 <ATK>
 A:Cross-references: GB:M69053; NID:q158468; PID:q158469
 R:Adelman, J.P.; Shen, K.Z.; Kavanaugh, M.P.; Warren, R.A.; Wu, Y.N.; Lagrutta, A.; Bond
 Neuron 9, 209-216, 1992
 A:Title: Calcium-activated potassium channels expressed from cloned complementary DNAs.
 A:Reference number: JH0697; MIMD:92360298
 A:Accession: PS0444
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 633-679 <ADE>
 C:Comment: This potassium channel is activated by calcium.
 C:Genetics:
 A:Gene: FlyBase:slo
 A:Cross-references: FlyBase:Fgn0003429
 C:Keywords: alternative splicing; ion channel; potassium channel; transmembrane protein

Query Match 34.9%; Score 1995; DB 2: Length 1184;
 Best Local Similarity 38.0%; Pred. No. 6.9e-132;
 Matches 436; Conservative 189; Mismatches 353; Indels 168; Gaps 18;

QY 27 FILSSFTVFFSGLLILFLRI-----WRSVKWQIINKGTGIIILE 66
 Db 36 FILSSITFLAGLLVLMRAFVCCRKPELDGPNPKQEKQAKNNKQEGEST----- 90
 QY 67 LFTSSGTARSHVRLHVGQGFROHIELMSAQTFVGQVILVVLVLSIGLITIFIN-SA 125
 Db 91 -----FMTEKDKWAGELISQTTTGRLVVLVILIASLITIFEVASS 134
 QY 126 DPVGSCTSYEDK-TIPIDLNVNAFFSYFGLRFMAADDKIKFEMLEMSIVDIPTPI 184
 Db 135 EBYVRCKCKMSNNITQOIDLAFNIFFWYFTRIRFASDKLMFEMKSFVDYFTIPSPFV 194
 QY 185 SYVUKSMWGLRFLRALRLLEPOILOILRAIKTSNVKFSKLLSITLSTWTAAGTILH 244
 Db 195 SIYLDRTWIGIRFLRALRLMTVPIQLYLWLKSSSIRLAQLVSIYSVWLTAAGTILH 254
 QY 245 VENGSDGWLGRNSQNTSYFESITLVMAATSTVGEGDVAAKTSIGRTIMEFTLGSILF 304
 Db 255 LENSGBP-LDFDNHRLSIWTVCYFLVLTWSTVGVDYCEYVGLRITFLVFEFLVLGAMF 313

QY 305 ANYIPEWVELFANKRKYTSSYEALGKRFIVYVCGNITVDVTAFLRNLDRKSGEINTEI 364
 Db 314 ASSIPEITELVSGSNKYGGLREKRGKRHLVYVGHITVESYHKLQFLEHREDVDVVEV 373
 QY 365 VFLEGTPPSLELETIFECYLAATYTFISGSAKMKEDLRVAVESAECLLIANPLCSDSA 424
 Db 374 VFLHRKPPDELEBGLFRHFTVVEFFQGTIMNPIDLORVYVHEADCLVLANKCCODPDA 433
 QY 425 EDISNIRVATSIKRYDSTTRITIOILSHKVVYLPKIPSNMWDGDNILICPAELKGFIA 484
 Db 434 EDANIMKRVATSIKRYSDDIRVITQIMQYHNKAVYLITPSDMKOGDDVITCLAEKLGFIA 493
 QY 485 QGCLVPLGCTFLSLFVEONKKVMP-KQTKKHFNLMSKKKILTLQRLSDDFAGMSPEVA 543
 Db 494 QSCLAPEFSTMMANLFLMRSPKTSPOQMSWTNDLRTGCMENYETISLPFFIGIPFQAT 553
 QY 544 RLCPFLKMYLLIAIEYVSLFTDGFGLNPPPOVRIRKNTLGFETPEKDVRAALFYC 603
 Db 554 ELCPSKLLLLAIEIKGA-BEGADSKISINPRGAKIQANTQGFIIQSADEVKRAMFYC 612
 QY 604 SVCHDDVFIPELTYNCCGKS-----RSR-----OHITVPS----- 633
 Db 613 KACHEDIKDELTKCKCKMLVQPRSKFDLDLHNPAFTTPELPKRVNHRGVSVDI 672
 QY 634 -----VKRMKCKLGISSR 647
 Db 673 TRQREDTNLNRNVRNRNGTNGTGMHNNNTAAAAAAGKQVKKKAPTY-NYSRQ 731
 QY 648 ISGO-DSPPRYASTSSISNFTT-----RTLDHVDQSDQLDSSGMFH 690
 Db 732 VEGGVISPSQYNRPRTSSSGTGNONGVSLPAGIADDSKDFPEKTEKKYDSTGMFH 791
 QY 691 WCKRTSIDKTYLTKTGSKYKFRNHIVACYVDGADHSAPKGLRNVMLASNTYRKELKD 750
 Db 792 WSPAKSLDEDCLIDNQAMTVLNGHVVCLEFADDSPLIGRLNLYMPLRASNFHYHELKH 851
 QY 751 IVFISGLDYLOREWRFLRNPQIYILPGCALYSGDLAANIEQCSMCALVSPRPQSSNQ 810
 Db 852 VVIYGSVDYIRREKMKIQLNPKISVYLVNGSPSLSRADLRVAVNNLCDKCCILSAKPSDDP 911
 QY 811 TLVDTEAIMATLTIGSLQID-----SSDPSVSEETPGYTNHNEKS 854
 Db 912 TLADKEAILASLNIAKAMFTDITIGVLSQGRPEFNDLSATAGSPIYQRR-GSYVGAN--- 967
 QY 855 NCRKVPILTELKNPSNIHFIEOLGCGSLQOETMLHLSTAFSTVSSSFLDSLATAF 914
 Db 968 ---VPMITELVNDGNGVQFLDQ---DDDDPDTLEYLTQPFACGTAFAVSVLDSLMSTTY 1020
 QY 915 YNYHVELLQMLVTVGVSSQLEQHLDRKQYGVADVASCSTLSGGRKCKIGLSLHETILS 974
 Db 1021 FQNALTLIRSLITGATPELELLAEGAGLRGYSVESLSNDRCRVGOISLYDGPILA 1080
 QY 975 DVNPRNTFGQLFCGSLDLFGILCYGLYRIID-EELNPNKRFVITRPNNEFKLLPSDLV 1033
 Db 1081 QFGECGYGDLFVALAKSYGLCIGLYRFRDTSSSCDASSKRYITNPDPDFSLPTDQV 1140
 QY 1034 FCALPF 1039
 Db 1141 FVLMOF 1146

RESULT 7

T27083
 hypothetical protein Y51A2.19 - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 R:McMurray, A.
 submitted to the EMBL Data Library, January 1998
 A:Reference number: Z20307
 A:Accession: T27083
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA


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Db      316 NGESHVAVYITTTLEEFIDLEEFAPRNO-RIQIVLL--SPALDQTMILKIPL 372
      385 --AYTFISGSAMKMEDLRVAESAACLIIANPLCSDSHADISIMVLSIKNDST 442
      373 WNNRVHNVYRSSLRDELEARNATSKACITLSARHNKRVATDEHTILSMKIKDAPN 432
      443 TRIIIOLOSHNKVYLPKIPSMMDTGDNITICFAELKLGFIAGCGLVGLCTFLTSLEVE 502
      433 VKQYVOIFRAETKMH1-----EHAEVLICDEFEYALANNCICPGISTFTLLMHT 484
      503 QNKKVMPKOT--WKK-----HFLNSM--KNKILIQRLSDDFGMSPEPARICFLMKYLLI 555
      485 SREBEGOKSTEPNKKYGFHSGNEMYOIKVODSKFCEYVGSFSTSPHAKHEYIGLI 544
      556 AIEYKSLFTDGFSG--LILNPPQVRIKNTLGFPIA---ETPRDYRALFYCSVCHDV 610
      545 AVS-----PDGDTSRMKLNGSHIIQPTDYVYMGLTNESLIDPRKGI---RSQOKRA 596
      611 FIEELLTNGCC-----KSRSHQITVPYVKRMKC-----LKGISRIISGODSPRVS 659
      597 NVASTIANIGTVAVDYPRSDKTELVGKRRKREKADEIHLIEVEGHVQSSRRPSIAY 656
      660 STSISNFTTR-----TLQHDVRODSQDQ-----DSSGMFMCKP-----TS 696
      657 TEGRIDSSSDDEICDRCGRPCIOHKLQRTYPOVRTYIGTSNTVCCHMKERRSLCCLK 716
      697 LDKVTLKRTGKS--KYKFRNHIVACVGDASHAPMGLRNFVMPLRASNTYRKELKDIV-- 752
      717 LDKCAHKSAHSAHEQWRNRPIILA--ADRTSSGMYNLVILRAYRVVHDLHPIL 773
      753 -----FIGSLDYIQREMRFLRNPQIYILPG-----CALYSGDLHAANIEQC 794
      774 LELEODSLNDAFLDAISY-----FPDYVMKMGKGNLDCLLRAGVSSAEHVVV 823
      795 SMCAYLSPRPQSPSSNOTVOTVEAIMATLTIGSLQIDSSSPSPSVSEPTGYTNGHNKS 854
      824 KETAVMAEHTADCN--TIIVQKIHRRFP----- 851
      855 NCRKVPILTELKPNINHFIE-----QLGLESLQETNLHL-----STAFSTGTV 901
      852 ---RLMITELTHATNMRFQFNPHNAVSLAOSRFEKKEKRSNHPMRFLRFAQGV 908
      902 SSSFDSLATAFAYNYHVELLQMLVYTGVSQLEOHLDKQYGVADSCSTLSLGRNRC 961
      909 SAMMDRLRLQALIKREVVLDVRLLL-----GIDQSDG----- 942
      962 KICGLSLHETILSDVNPRTFGLF---CGSLDLFGILCYGLYRI-----IDEEEL 1009
      943 --GYLTSFVITSDMLIRN--YGRILYOKLSSV---ADIPIGITRTKKMDTKTYVSLDLEQ 996
      1010 NPNKRFVITRPAHEKLLPSDLVFCALPESTACYRNEEFSLOKSEIYNKASQTTEDT 1069
      997 CKPFENTEMGRNKMVDYHVNRRRLNIKQTHLLLEGSDKS--QISVIINPAODL---- 1051
      1070 FRHKLSSHPLQLLRHCINOSILTSR 1095
      1052 ---ELESGDIVYIRSPIRKDATNAR 1074

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RESULT 11

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T20577
hypothetical protein F08B12.3a - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C:Accession: T20577
R: Dobson, R.
submitted to the EMBL Data Library, November 1995
A: Reference number: Z19295
A: Accession: T20577
A: Status: preliminary; translated from GB/EMBL/DBJ
A: Molecule type: DNA
A: Residues: 1-1119 <M1>

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A: Cross-references: EMBL:Z68104; PIDN:CAA92115.1; GSPDB:GN00028; CESP:F08B12.3a
A: Experimental source: clone F08B12
C: GenBank:
A: Gene: CESP:F08B12.3a
A: Map position: x
A: Introns: 38/2; 64/1; 112/2; 148/3; 173/3; 201/3; 348/3; 392/2; 452/1; 488/2; 538/2;

Query Match      6.3%; Score 361; DB 2; Length 1119;
Best Local Similarity 20.4%; Pred. No. 5,1e-17;
Matches 228; Conservative 179; Mismatches 424; Indels 286; Gaps 48;

      101 VGOVLVIVLVLST--GSLIYFINSADPVGSCSYEDKTPIDLVENAFPSYFGLREMA 159
      134 ISMYVTLVFLVLSYSGSVRLIN-----IHFLLELTLSFPF----- 170
      160 ADDKIKFMLEMNSIVDTFTPR-----PFIISYLLKSNMLGRLFRALRLLLEPQILOI 212
      171 -----LISIF--IPSLITYLVFVFLNC-----WLAGALQAM-----MNDL 204
      213 LRAIKTSNVKFSKLL--SIILSTWETAAGT--HLEVNSGDPMLKGRNSQISYESIY 268
      205 NRSFSSSALFQRLLLFVLACLIFTGMCSTIEHLQIRANG-----KRIDLFTSEY 255
      269 LVNATTSTVGEGDVAKTSLGRTIFEFYGLSLILPANTYIPENVELFANKRKYTSYEAL 328
      256 FVMVTFSTVGDMYPRDYMASQLCVLLICVALGLIPKQDELQGTWSEHOKSGTGFSSW 315
      329 KG--KKFIYVCGNITVDSVAFILRNLFRDKSGETMEIVLFGTTPSLEET--IFRCYL 384
      316 NGESHVAVYITTTLEEFIDLEEFAPRNO-RIQIVLL--SPALDQTMILKIPL 372
      385 --AYTFISGSAMKMEDLRVAESAACLIIANPLCSDSHADISIMVLSIKNDST 442
      373 WNNRVHNVYRSSLRDELEARNATSKACITLSARHNKRVATDEHTILSMKIKDAPN 432
      443 TRIIIOLOSHNKVYLPKIPSMMDTGDNITICFAELKLGFIAGCGLVGLCTFLTSLEVE 502
      433 VKQYVOIFRAETKMH1-----EHAEVLICDEFEYALANNCICPGISTFTLLMHT 484
      503 QNKKVMPKOT--WKK-----HFLNSM--KNKILIQRLSDDFGMSPEPARICFLMKYLLI 555
      485 SREBEGOKSTEPNKKYGFHSGNEMYOIKVODSKFCEYVGSFSTSPHAKHEYIGLI 544
      556 AIEYKSLFTDGFSG--LILNPPQVRIKNTLGFPIA---ETPRDYRALFYCSVCHDV 610
      545 AVS-----PDGDTSRMKLNGSHIIQPTDYVYMGLTNESLIDPRKGI---RSQOKRA 596
      611 FIEELLTNGCC-----KSRSHQITVPYVKRMKC-----LKGISRIISGODSPRVS 659
      597 NVASTIANIGTVAVDYPRSDKTELVGKRRKREKADEIHLIEVEGHVQSSRRPSIAY 656
      660 STSISNFTTR-----TLQHDVRODSQDQ-----DSSGMFMCKP-----TS 696
      657 TEGRIDSSSDDEICDRCGRPCIOHKLQRTYPOVRTYIGTSNTVCCHMKERRSLCCLK 716
      697 LDKVTLKRTGKS--KYKFRNHIVACVGDASHAPMGLRNFVMPLRASNTYRKELKDIV-- 752
      717 LDKCAHKSAHSAHEQWRNRPIILA--ADRTSSGMYNLVILRAYRVVHDLHPIL 773
      753 -----FIGSLDYIQREMRFLRNPQIYILPG-----CALYSGDLHAANIEQC 794
      774 LELEODSLNDAFLDAISY-----FPDYVMKMGKGNLDCLLRAGVSSAEHVVV 823
      795 SMCAYLSPRPQSPSSNOTVOTVEAIMATLTIGSLQIDSSSPSPSVSEPTGYTNGHNKS 854
      824 KETAVMAEHTADCN--TIIVQKIHRRFP----- 851
      855 NCRKVPILTELKPNINHFIE-----QLGLESLQETNLHL-----STAFSTGTV 901
      852 ---RLMITELTHATNMRFQFNPHNAVSLAOSRFEKKEKRSNHPMRFLRFAQGV 908
      902 SSSFDSLATAFAYNYHVELLQMLVYTGVSQLEOHLDKQYGVADSCSTLSLGRNRC 961

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Db 909 SANMLDRLLYGAIIRKPFVVDLVRLL-----GIDQHS DG----- 942
Oy 962 KLGSLSHETLSDVNPNTGOLF--CGSLDFGLICVGLYRI--IDEE---ELNPE 1012
Db 943 --GILTSFVITSDMLWLN-YGRLOXKLCSSV---ADIPGIFRKKMDKTFVSLDLOEQ 996
Oy 1013 NKRRVITRPA-----NEFKLLP-SDLVECAIPSTGACYNKEEFSLOK---SYEI 1058
Db 997 CKDENTENMGKNNKMDYKABKRNRLNLIKDTHTFNMKATASCRSTVLEGSDEKSOISYI 1056
Oy 1059 VNKAQOTEDTFRHKLSSHPILQLRHCIHQSIILTSR 1095
Db 1057 INPADL-----ELESGLIYVIRSPIDRKDATNAR 1086

RESULT 12
T02865
calcium activated potassium channel CACK1 [Imported] - Leishmania major (strain Friedlin
C:Species: Leishmania major
C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 19-May-2000
C:Accession: E81464; T02865
R:Myler, P.J.; Audleman, L.; devos, T.; Hixson, G.; Kiser, P.; Lemley, C.; Magness, C.;
Proc. Natl. Acad. Sci. U.S.A. 96, 2902-2906, 1999
A:Title: Leishmania major Friedlin chromosome 1 has an unusual distribution of protein-c
A:Reference number: A81455; MUID:99178987
A:Accession: E81464
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1017 <PVL>
A:Cross-references: GB:AE001274; NID:93264850; PIDN:AC24688.1; PID:93002487; GSPDB:GNOC
A:Experimental source: strain MHOM/IL/81/Friedlin
A:Genetics:
A:Gene: CACK1
A:Map position: 1

Query Match 5.5%; Score 316.5; DB 2; Length 1017;
Best Local Similarity 19.9%; Pred. No. 6e-14;
Matches 204; Conservative 154; Mismatches 437; Indels 229; Gaps 39;

Oy 141 IDLVFN-AFESFYGLRPMADDK--IKFWLEMSIVDIFPTPTF---ISYYIKSNMLG 194
Db 96 VELVLSIFFLAWGLFFEPEDKAYLISWL---SLVNAMTISPMIVIGIGALKDSSWS 152
Oy 195 LRFRLAR-----LLELPOLQLLRKITSNSVKFSLLSIIISTWTAGFIHL 244
Db 153 VWVPWYLVWMLCDCLSVLIDVPOIARHTPEKWRMRYFIRLFVVC---TCVGTQOI 208
Oy 245 VENSQDPMKGRNSQNIYSFESIVLWMTTSTVGQDVAAVATSLGRFTIMFTGLSLIF 304
Db 209 VESGCGV-----VDLYDSLYIIVAFNITIGRGDTAFTTPARIMIAFIVIGICFF 260
Oy 305 ANYIP--EMVELPANKRYTSSYE-----LNGKK--FIVYCGNITVDSYTAFLRNFL 353
Db 261 --LPLFRLSVIARSOLOHTMTFSGSGSASWLRGMKHPHYICQFSDLSLELLRNFY 317
Oy 354 RDKSEINTETVFLG--ETPPSELETIFKCYLAATTFISGAMKMWELLRVAVESAEAC 411
Db 318 AGMKRYLDTCTVLAPREHSPREVLAAANLPMWLGKRYTLVAGDPAPKDKAKADADA 377
Oy 412 LIANPLCSDSHADISNIMRVLSIKNYDSTRIITIIQLGSHNKYYLKPISMNMDTGDN 471
Db 378 FLFGGRS-STAYVDYTIILASVANSKYD---RNLPQHLLHNRCTVQOISY-----AAS 429
Oy 472 IICRAELKGLTACGLVIGICTFLTSL--FVEONKKVMPKQTKKHFHLSMKKILITQ 528
Db 430 VLEVERIILHLLGLISMARPGVPLVNLRTYESLPDITLSRHVWEQYEYSLRNDMGL 489
Oy 529 RLSDQFAGMSPEVARLCEFLKMYLLILAIKYSKSLFTDGFGLILNPPQVARRKNTLGF 588
Db 490 ELPDLKRREFVLAARSFEEDVDTLIGILNRSV-----VOLNPRELVNPAKRLI--L 540
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Oy 589 IAETPKDVRALFCSYCHDDVFIPELIT-----NCGCKSRSRHOITVPSVKRMKCL 641
Db 541 IAKTKVAQADATDAIARHEOTFGEMLAAPDPDEHDAKRRARRRRLVILBRSSSSSS 600
Oy 642 KGISRSIGQDSPR-----VSASTSSISNFTTLOHDE----- 677
Db 601 SGVDQVEDRNGAPRGDRMPROTAAHVASASRAPATPTTIDTSQRTQVRRPAAAAALEN 660
Oy 678 -----QSDQDSSGMFMKCPISLDKY-----TLKR 704
Db 661 NGGLARAPPVSVLHPSSGSSIAAEGSSGDEFDARSIVAASPSBPPSRRAPVRSEALVR 720
Oy 705 TGSKSKYKRNHIVACVFSDAASAPWGLR-----NFVMPLRASNTYRKL- 748
Db 721 IDDA-FDLENHFPVYVDDSSAKADESSRYAGEAVNTAAHDFHTVMTVROA-YRANIV 778
Oy 749 --KDIVEIGSLDYLRQREFLRNPQIYILPGCALYSGDLHAANI EOCSSMCVAVLSPPO 805
Db 779 LLTNDVSEGPLDYVSWVHRODSANPVKYI--SGCGLNTADLRRCMLERCACCVFAGDV 837
Oy 806 PSSNOTLVDTFAIMATLITGSLQIDSSDPSPSVSEETPGYTNKINENKRPVIL--- 862
Db 838 SRSGST-----SAMSILVLSINETLHGIRPAVPVVEGLAN-----LPLFPPH 882
Oy 863 --TELKNPSNIHFEOGLGEGSLQETNHLSTAFSTGTFSSSFLDSLATAFVYNHV 919
Db 883 AEDLRKTRKAELDFY-----YEPN-----FITGNVSRMLPLPALQRTYFMEEF 926
Oy 920 LELLQMLVTVGGVSSOLEQHLDKRYGVAVDSCTSLSSGRNCKLGLSLHETIISDVNR 979
Db 927 IDVMVLVLSGHAPD-----TPALA--RLPLSLFOAEIQTYEDV--- 962
Oy 980 NTFQGLFCGSLDRCILCVGLY-RIIDEEELNPEKKRVRTPRANEFLLP-----SDLVF 1034
Db 963 ---VVYCLK--FGYLPALQRIVDVNPDSINCGRVFLTPP--RALPVNOQTDLF 1012
Oy 1035 CAIP 1038
Db 1013 YTP 1016

RESULT 13
T02866
hypotheical protein CACK2 [Imported] - Leishmania major (strain Friedlin)
C:Species: Leishmania major
C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 19-May-2000
C:Accession: E81464; T02866
R:Myler, P.J.; Audleman, L.; devos, T.; Hixson, G.; Kiser, P.; Lemley, C.; Magness, C
Proc. Natl. Acad. Sci. U.S.A. 96, 2902-2906, 1999
A:Title: Leishmania major Friedlin chromosome 1 has an unusual distribution of protei
A:Reference number: A81455; MUID:99178987
A:Accession: E81464
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1159 <PVL>
A:Cross-references: GB:AE001274; NID:93264850; PIDN:AC24688.1; PID:93006218; GSPDB:G
A:Experimental source: strain MHOM/IL/81/Friedlin
A:Genetics:
A:Gene: CACK2
A:Map position: 1

Query Match 4.7%; Score 270; DB 2; Length 1159;
Best Local Similarity 16.5%; Pred. No. 1.4e-10;
Matches 194; Conservative 178; Mismatches 442; Indels 360; Gaps 38;

Oy 63 IILEFTSGTARS-----HVRSLHFOGFRDHIMLSAQTFVGOVIVLVLSIGSL 117
Db 139 ILLILCNVGLAARAGCIVLHVQNAHVTAQDMR---EFDGICGFIAFVLLSVFMSWSTL 195
Oy 118 II-----YFINSADPYGSCSYEDKTIPIIDLVNAAFFSYFGLRPMADDKIKFWLEM 170
Db 196 LAVEAKKNVYLVNARSLSMNYLSS-----GMWLL 223
```

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OY 171 NSYDIFPTPTISY-----LKSNIUGLRLRLLELPQIQLIRAITSNSVFSK 226
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 224 LALALLTLDRAMTHVAPMFLRYMML-----HESLISLNYPOI-----SVYTERLEKVR 276
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 227 LSLILSWFAAGFIHLVEN-SGDPMLKGRNSONISFESIYVMATTSVSGDVAK 285
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 277 SMTGCIANVGISVGLAVESFCGP-----VEFDMVMMLLSFSSIGDVTPL 327
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 286 TSLGRTFIMFTGLSLILFANYIPEWELFANKRRYTSY-----EALGKKFIYVCGNIT 341
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 328 TVGGRLLMIIF-IG-VGFSYFV-ILQYVADLVHLSAVYTCFERIDHVICGHLG 383
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 342 VDSYATLRLNFKRSGEINTIYFLGEPPELLETIFEC--YLAITYTISGAMRWED 399
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 384 YNEIRMLCKNFADRYHLNMSVLLREOPSQVLLILNSPKYRSVHLLVYCGVPTD 443
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 400 LRRVAVSAAEACLIANPLGSDSHAEISNMRSLSTKNDSTRITIIQLQS-HNKVYL 458
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 444 LDRGNANGA-AAMP/LGAGTNSYSYSD/LAQMVTNALVPL/LYLRLHRSYTSLSM 502
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 459 PKIPSMMDTGNICEAEKLGFIAGCLVPGCLTFELTSFVEQNKVMPKQTKKHF 518
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 503 P-----SRAIYLFERLHNHNLGLGCVLPGMIPLVANLM-----RMF 539
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 519 NSMKKILTO-RISDDFRAGNSFPEVARLCEKMTLLALIEYKSLFTDGCGLILN--- 573
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 540 DPMTEALMELRDEKDLGLSGSNAASLRAMKMW-----APKRPMLYGAATIELGLAE 594
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 574 -----PPQVR-----IRKNTLGFPIAE 591
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 595 PDMNSTEASLAQHVDAVAPRPVQRGHYVYRLARLLRYNITLIGVNSSGCGDSVYE 654
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 592 -TPK---DVRALFEGSV--CHDVEIPELITNGCKSRSROHITVSVYKMKCKLGI 644
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 655 LAPGSLVYKLLIVICDVRRAQDI-VDEIVNDATRGSTSSAAGAPAIR----- 704
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 645 SSRTSGDSPRVSATSSSI-----SNFTTRITQ----- 673
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 705 -----SPRPAGVQATVAVVPIPAKEDAGAVMNSSTTTTIAPARASQMLKPA 756
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 674 -----HDV-----EODSDQLSS 686
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 757 PAPATATVIGASAVELPRRLRHVACERAAEARMHNDSSLYLSAATAEDDDDEDA 816
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 687 GMEHMKPTSLDKV-----TLKRTGSKYKFRNH 715
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 817 LIGALAPVLLDAVGRGRPACVDARVGPATVSPSLVFAAAAHSYLVRPDRHLANH 876
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 716 IVACVFGDAHSAPKGLRNFVPLR--ASNY-----TRKELK--IVFTG--SLDYLO 761
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 877 YVFIDLSAHERTNMSREAAVESRTAKAADYIDIMRPVROHDPDSNIVLLANDTNYDSL 936
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 762 REMHFLNFPQIYLLPGCALYSGDLHAANIEQCSMACAVLSPPOPSNQTLVDTEAIMAT 821
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 937 NMMEEDVNTSLIYVCGCGFTSDLRRCNTKAAAIYIFAGDGCDEHG--DLSLVLM 993
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 822 LTGSLQIDSSDPSVSEPTGYNGHNEKSNCRKVPILTELKPNSHIFEQGLGLE 881
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 994 QLVROL-----IGEDRHGSAADIPYIEVDHAEIPLFAPAMTLG 1033
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 882 GSIQETNLHLSAFTGTVSSSFLDSLATAFYNHVLELLOWLGVGSSOLEQHLDK 941
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1034 KDVAAMAVLEPMSVSCVCRHMLDTGLQDMFTPELADVLLEOLSSKESLSLVYMAP 1093
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 942 DKYVGVADSTSLSGNRNKLGLSLHETILSDVNPNTFGOLFCSLDLFGILCVGLY 1001
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1094 DAAMTVEDATSGIDGSLPLAIHREHMIRODTS----- 1129
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 1002 RIIDEEELNPKRFVITTPRANFKLLPSDLVFC 1035
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1130 -----VSFRYITNPPSPFPLHDDFIYC 1153
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```

RESULT 14
C64317
hypothetical protein M0139 - Methanococcus jannaschii
C:Species: Methanococcus jannaschii
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C:Accession: C64317
R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blak
; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weissbrock, K.G.; Merrick, J.M.; Glodek,
; rson, J.D.; Sadov, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
; Science 273, 1058-1073, 1996
A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Frazer, C.M.; Smith, H.O.; Woese
A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannasc
A:Accession number: A64300; M01D:96337999
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-209 <BUL>
A:Cross-references: GB:067471; GB:L77117; NID:92826249; PIDN:AB98122.1; PID:91498908
C:Genetics:
A:Map position: FOR136616-137245

Query Match 3.88; Score 216.5; DB 2; Length 209;
Best Local Similarity 25.98; Pred. No. 6.3e-08;
Matches 60; Conservative 55; Mismatches 80; Indels 37; Gaps 7;

OY 103 QVILVFLVLSIGSLIYFINSADPVGSSSEDKTIPIDLVNAPFSYFGLRFMAAD 162
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 10 KIMVLSLITFFELVASFILSTNMP-----PYQDLIKLDIISIMTFTEIYFVYED 64
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 163 KIKWLEMSIVDIETTPPTFISYLLK---SNWGLRFLRALRLLELPQIQLIRA 218
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 65 KAKFFKDIYVDAIV-IAFLYSLQVFSKAFGLRVIMLRILVLRITKRLKEEN 123
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 219 SNSVFKSLIISLWTFAGFHLVENSQDPLKGRNSONISFESIYVMATTSVG 278
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 124 QALINFLTLITC-----FISCLTIWESGVNPAIN-----NEFDNFPTTISTITVG 172
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 279 FGDVVAKTSIGRTFIMEFTGLSLILFANYIPEWELFANKRRYTSYEAALG 330
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 173 YGDITPPTDAGKLITIF-----SVLFISGL-----ITSLKALKG 208
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 15
A70461
potassium channel protein - Aquifex aeolicus
C:Species: Aquifex aeolicus
C:Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 05-Nov-1999
C:Accession: A70461
R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.;
V. Nature 392, 353-358, 1998
A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A:Reference number: A70300; M01D:98196666
A:Accession: A70461
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-455 <AO>
A:Cross-references: GB:AE000760; NID:92984138; PIDN:AAC07678.1; PID:92984143; GB:AE00
C:Experimental source: strain VFS
C:Genetics:
A:Gene: Kch

Query Match 3.7%; Score 209.5; DB 2; Length 455;
Best Local Similarity 25.18; Pred. No. 6.1e-07;
Matches 99; Conservative 69; Mismatches 148; Indels 79; Gaps 18;

OY 92 EMILSAQTFVGQVL-----VILVFLVLSIGSLIY-----FINSADPVGSSSEDKTIP 140
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 7 ELLEDRSFVFYIYNFSSFVILISVI-----LTLYDFYGFHSLKRPV-----VLE 53
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```


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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 5, 2001, 12:03:42 ; Search time 57.65 Seconds
(without alignments)
1162.004 Million cell updates/sec

Title: US-09-176-664-16
Perfect score: 5722
Sequence: 1 MFQTKRNETMEDLPKMSCT.....CIHQSLTSLRELPPLFLSK 1105

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

A_Geneseq_0601:*

- 1: /SIDS8/gcgdata/geneseq/geneseq/AA1980.DAT:*
- 2: /SIDS8/gcgdata/geneseq/geneseq/AA1981.DAT:*
- 3: /SIDS8/gcgdata/geneseq/geneseq/AA1982.DAT:*
- 4: /SIDS8/gcgdata/geneseq/geneseq/AA1983.DAT:*
- 5: /SIDS8/gcgdata/geneseq/geneseq/AA1984.DAT:*
- 6: /SIDS8/gcgdata/geneseq/geneseq/AA1985.DAT:*
- 7: /SIDS8/gcgdata/geneseq/geneseq/AA1986.DAT:*
- 8: /SIDS8/gcgdata/geneseq/geneseq/AA1987.DAT:*
- 9: /SIDS8/gcgdata/geneseq/geneseq/AA1988.DAT:*
- 10: /SIDS8/gcgdata/geneseq/geneseq/AA1989.DAT:*
- 11: /SIDS8/gcgdata/geneseq/geneseq/AA1990.DAT:*
- 12: /SIDS8/gcgdata/geneseq/geneseq/AA1991.DAT:*
- 13: /SIDS8/gcgdata/geneseq/geneseq/AA1992.DAT:*
- 14: /SIDS8/gcgdata/geneseq/geneseq/AA1993.DAT:*
- 15: /SIDS8/gcgdata/geneseq/geneseq/AA1994.DAT:*
- 16: /SIDS8/gcgdata/geneseq/geneseq/AA1995.DAT:*
- 17: /SIDS8/gcgdata/geneseq/geneseq/AA1996.DAT:*
- 18: /SIDS8/gcgdata/geneseq/geneseq/AA1997.DAT:*
- 19: /SIDS8/gcgdata/geneseq/geneseq/AA1998.DAT:*
- 20: /SIDS8/gcgdata/geneseq/geneseq/AA1999.DAT:*
- 21: /SIDS8/gcgdata/geneseq/geneseq/AA2000.DAT:*
- 22: /SIDS8/gcgdata/geneseq/geneseq/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	5722	100.0	20	AAV13442
2	5573	97.4	20	AAV13443
3	3717.5	65.0	20	AAV13437
4	2350	41.1	20	AAV32017
5	502	112	20	AAV13439
6	496	8.7	20	AAV13438
7	493	8.6	20	AAV13440
8	491	8.6	20	AAV13441
9	169	3.0	20	AAV132012
10	168	2.9	20	AAV50342
11	158.5	2.8	20	AAV32015

12	154.5	2.7	519	21	AAV44565	Human Voltage-gate
13	154.5	2.7	519	21	AAV44569	Human Voltage-gate
14	154.5	2.7	519	21	AAV44570	Human Voltage-gate
15	154.5	2.7	519	21	AAV44571	Human Voltage-gate
16	154.5	2.7	519	21	AAV44572	Human Voltage-gate
17	152.5	2.7	466	20	AAV50341	Human Kv6.2 protel
18	147.5	2.6	506	21	AAV44568	Mouse Voltage-gate
19	147	2.6	857	20	AAV32019	Arabidopsis thaila
20	145.5	2.5	477	20	AAV34127	Human potassium ch
21	145.5	2.5	506	21	AAV44564	Mouse Voltage-gate
22	145.5	2.5	506	21	AAV44566	Mouse Voltage-gate
23	145.5	2.5	506	21	AAV44567	Mouse Voltage-gate
24	145.5	2.5	655	19	AAW79590	Human Kv potassium
25	143.5	2.5	676	21	AAV57368	Human KVLQT1 prote
26	143.5	2.5	676	21	AAV80562	Human long QT synd
27	143.5	2.5	676	22	AAV89494	Human KVLQT1. Hom
28	143	2.5	677	20	AAV08343	Human KCNQ1 protel
29	141.5	2.5	630	20	AAV13523	Human amino acid sequenc
30	141	2.5	873	21	AAV97876	Eucaalyptus camalidu
31	140	2.4	824	20	AAV24001	A potassium channe
32	139.5	2.4	616	20	AAV32013	Drosophila melanog
33	139	2.4	636	19	AAW79589	Human Kv potassium
34	138.5	2.4	376	18	AAW50036	Xenopus KVLQT1. X
35	138.5	2.4	376	21	AAV57376	Xenopus KVLQT1 par
36	138.5	2.4	376	21	AAV80567	partial Xenopus Kv
37	138.5	2.4	988	22	AAV31714	A human alpha-subu
38	138	2.4	1017	20	AAV22427	Human brain specif
39	137	2.4	495	20	AAV33766	hkv3.1 human brain
40	137	2.4	513	17	AAV90764	Human K+ channel 1
41	137	2.4	513	19	AAW42995	Putative mature po
42	137	2.4	636	19	AAW79591	Human Kv potassium
43	136	2.4	499	20	AAV34122	Human potassium ch
44	136	2.4	646	20	AAV34123	Human potassium ch
45	135	2.4	662	20	AAV14585	A.thaliana potassl

ALIGNMENTS

RESULT	1
AAV13442	
ID	AAV13442 standard; Protein: 1105 AA.
XX	
AC	AAV13442:
XX	
DT	26-JUL-1999 (first entry)
XX	
DE	Amino acid sequence of hsl03-1.
XX	
KW	Voltage-gated; pH sensitive; potassium channel; sl03; spermatocyte;
KW	sperm capacitation; acrosome reaction; fertilization; infertility;
KW	contraceptive; sperm physiology; channel protein; gene therapy.
XX	
OS	Homo sapiens.
XX	
PN	W09920754-A1.
XX	
PD	29-APR-1999.
XX	
PF	21-OCT-1998; 98WO-US22321.
XX	
PR	27-FEB-1998; 98US-0076172.
XX	
PA	22-OCT-1997; 97US-0063138.
XX	
PI	(UNIW) UNIV WASHINGTON.
XX	
DR	Salikoff L, Schreiber M, Silvia C;
XX	
DR	WPI: 1999-326593/27.
XX	
PT	N-PSDB; AAX55524.
XX	
XX	Voltage-gated, pH-sensitive potassium channel useful in gene therapy

PS Claim 1; Page 79; 93pp; English.
XX
CC The invention relates to a voltage-gated, pH sensitive potassium channel
CC S103, expressed in spermatoocytes. S103 has, as a monomer, calculated
CC molecular weight 120-156 kD; has unit conductance (as a functional
CC tetramer, when expressed in Xenopus oocytes) of 80-120 pS; has increased
CC activity at intracellular pH above about 7.1 and binds specifically to
CC polyclonal antibodies against sequences shown in AAY13437, AAY13438,
CC AAY13442, and AAY13443. S103 is involved in sperm capacitation and/or the
CC acrosome reaction, essential steps in fertilization. S103, and the
CC nucleic acid encoding it, are used to identify specific inhibitors and
CC activators (potentially useful for treating infertility and as
CC contraceptives), also for studying sperm physiology in vitro.
CC S103-specific antibodies are used for diagnostic detection of S103
CC expression. S103, as part of a chimera with another channel protein, can
CC be used as a reporter for measuring changes in potassium concentration,
CC current flow, ion flux, etc. Fragments of S103 nucleic acid are useful as
CC probes for identifying homologs, variants and mutants associated with
CC disease; to detect S103-related mRNA or protein; for chromosomal
CC localization; in gene therapy; for identifying potential modulators; to
CC measure up-regulation of S103 in drug screening assays and for production
CC of recombinant S103 protein. The present sequence represents the amino
CC acid sequence of hS103-1.
XX
XX

SO Sequence 1105 AA:

Query Match 100.0%; Score 5722; DB 20; Length 1105;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPTQKLKRNEMEDLPKMSCTTEIOAFLISFPTFFSGLIILILFLIKMSVKKMQIKG 60
DB 1 mptqklrnelwedlprkmsctteioaflisfptffsgliililflirsvrkwkqllkg 60
QY 61 TGIILEFTSGTARSHVRLHFGQFRDHEMLSAQTFVGQVLVLVLSIGSLIIT 120
DB 61 tgiilleftsgtarshvrlhfgqfrdhemlsaqtfvgvlylvvlvlsigslily 120
QY 121 FINSADPVGSCSSYEDKTIPIDLVFNAFSFFYGLRPMADDKIKFWLENNSTVIDFTIP 180
DB 121 finsadpvgscssyedktipidlvfnafsfyglrpfmaaddkikfwlennstvidftip 180
QY 181 PTFISYLYKSNMGLRFLRLRLLELPQIILRAIKTSNVSKLSIISTWTPIAAG 240
DB 181 ptfisylyksnmglrflrlrllelpqiilraiktsnvsklsisistwtftaag 240
QY 241 FHLVENSQDPMFKGRNSONISFEESIYLVMTTSTVGFDVAAKTSLSGRTFMFTIGS 300
DB 241 fhlvensqdpmlkgrnsonisfeesiylvmttstvgfdvvaaktslsgrtfmftlgs 300
QY 301 LILFANYIPBMVELFANKRRKRYTSSYEALNGKRFIVCGNITVDVYTAFLRNLDRKSGEI 360
DB 301 lilfanyipemvelfankrrkrytssyealngkrfivcgnitvdsytaflrnlrdksgei 360
QY 361 NTRIVLUGETPPBLEETFKCYLATTTTSSGAMKWEDEARRAVASAEKCLIANPLCS 420
DB 361 ntrivlugeppbleetfkcylattttssgammkwedearravasaecklianplcs 420
QY 421 DSHAEDISNIMRYLSIKNVDSTRIITIOLOSNNKYLLPKIPSMNDGTGNIICFAPLKL 480
DB 421 dshaedisnimrylsiknvdsttriiitioiosnnkyllylpkipsmndgtgniiicfapkl 480
QY 481 GFIAQGCCLVPGICTFLTSLFVEONKRYMPKQTKWKHFLNSMKKKILTORLSDDFAGMSFP 540
DB 481 gfiaqgcclvpgictfltslfveonkrvmpkqtkwkhhflnsmkkkiltorlsddfagmsfp 540
QY 541 EVARLCEFLKMYLLLIAIKRSLFTDGCGLIAPPPOVRIKRTTLCGFFIAETPKDVRRL 600
DB 541 evarlcefkmlyllliaikrslftdgcgcliapppovrirkttlcgffiaetpkdvrral 600
QY 601 FYCSVCHDDVFIPELITNCGCKRSRQHTVPSVKRMKKCLKISSRISGODSPRVSAS 660
DB 601 fycsvchddvfiipelitnccgckrsrqhtvpsvkrmkcklkiissrisgodsprvsas 660

DB 601 fycsvchddvfiipelitnccgckrsrqhtvpsvkrmkcklkiissrisgodsprvsas 660
QY 661 TSSISNFTTFTLQHDVEDSDQDSSGMFHWCKPTSLDKVTTLKRTGSKYKFFNNHIVACY 720
DB 661 tssisnfttftlqhdvedsdqddssgmfwckptsldkvtltlkrtgskykffnnhiyacv 720
QY 721 FGDASHAPKGLNFWPLRASNTYRKELADIVETIGSLDYLQREWRFLRNPQIYILPGCA 780
DB 721 fgdashapkglnfwplrasntyreladivetigsldylqrewrflrnpqiylilpgca 780
QY 781 LYSGDILHAANIEQSCMAVISPPOPSNOTVDFEAIMATLTIGSLOJDISSDPSPSV 840
DB 781 lysgdilhaanieqscmavispppsnotvdfaimatltigslojdissdpspsv 840
QY 841 EETPGYTNHNEKSNCRKVPILTELKNPSNIHPIEQLGEGSLQETNHLSTAFSTGTIV 900
DB 841 eetpgytnhneksncrkvpiltelknpsnihpieqlgegslqetnhlstafstgtiv 900
QY 901 FSSSFIDSLATRFYNYHVELLQMLVTGCVSSQLQHLDDKRYGVADSCISLSGRNR 960
DB 901 fsssfidslatrfynyhvelqlmlvtgcvssqlqhlddkrygvadscislsgrnr 960
QY 961 CKLGLSLHETIISDVNPRMTFGOLFCGSLDLFGIICVGLYRIIDEELNPEKKRFVTR 1020
DB 961 cklglslhetiiisdvnpmtfgolfcgslldlfgiicvglyriideelnpekkrfvtr 1020
QY 1021 PANEFKLPDSLVFCAIPSTACRYKRNEEFSLOKSYEIVNKAQOTTEDTRHKLSSHPLI 1080
DB 1021 panefklpdslvfcaipstacrykrneefslouksyevinkaqottedtrhklsshpil 1080
QY 1081 QLLRHCIHOSILRSRELTPSLFSK 1105
DB 1081 qlrlrhcihosilrsreltpslfsk 1105

RESULT 2

AAY13443
ID AAY13443 standard; Protein; 1081 AA.

XX AAY13443;

XX 26-JUL-1999 (first entry)

DE Amino acid sequence of hS103-2.

KW Voltage-gated; pH sensitive; potassium channel; S103; spermatoocyte;

KW sperm capacitation; acrosome reaction; fertilization; infertility;

KW contraceptive; sperm physiology; channel protein; gene therapy.

OS Homo sapiens.

XX W09920754-A1.

XX 29-APR-1999.

PF 21-OCT-1998; 98WO-0522321.

XX 27-FEB-1998; 98US-0076172.

PR 22-OCT-1997; 97US-0063138.

XX (UNITW) UNIV WASHINGTON.

PI Salzkoff L, Schreiber M, Silvia C;

XX WPI; 1999-326593/27.

DR N-PSDB; AAX55525.

XX Voltage-gated, pH-sensitive potassium channel useful in gene therapy

PS Claim 1; Page 81; 93pp; English.
XX
CC The invention relates to a voltage-gated, pH sensitive potassium channel
CC S103, expressed in spermatoocytes. S103 has, as a monomer, calculated

CC molecular weight 120-156 kD; has unit conductance (as a functional tetramer, when expressed in *Xenopus* oocytes) of 80-120 pS; has increased activity at intracellular pH above about 7.1 and binds specifically to polyclonal antibodies against sequences shown in AAY13437, AAY13438, CC AAY13442, and AAY13443. S103 is involved in sperm capacitation and/or the CC acrosome reaction, essential steps in fertilization. S103, and the CC nucleic acid encoding it, are used to identify specific inhibitors and CC activators (potentially useful for treating infertility and as contraceptives), also for studying sperm physiology *in vitro*. CC S103-specific antibodies are used for diagnostic detection of S103 expression. S103, as part of a chimera with another channel protein, can be used as a reporter for measuring changes in potassium concentration, CC current flow, ion flux, etc. Fragments of S103 nucleic acid are useful as probes for identifying homologs, variants and mutants associated with CC disease; to detect S103-related mRNA or protein; for chromosomal CC localization; in gene therapy; for identifying potential modulators; to CC measure up-regulation of S103 in drug screening assays and for production CC of recombinant S103 protein. The present sequence represents the amino CC acid sequence of hS103-2.

XX Sequence 1081 AA:

Query Match 97.4%; Score 5573; DB 20; Length 1081;
Best Local Similarity 97.8%; Pred. No. 0;
Matches 1081; Conservative 0; Mismatches 0; Indels 24; Gaps 1;

OY 1 MFQTKLNEMTEDI.PKMSCTTETIOAFLTSFVPFSGILILLIRLIWVSKWQITIG 60
1 mfgtklnetwedipkmscttelgaafllsftffsgllllllfrllwvskkwqikg 60
DB 1 TGIILLETSGTIRSHVRS.HFQGFDRHTEMLSAQTFFGVYLVILFVLSTGSLITY 120
61 TGIILLETSGTIRSHVRS.HFQGFDRHTEMLSAQTFFGVYLVILFVLSTGSLITY 120
DB 61 TGIILLETSGTIRSHVRS.HFQGFDRHTEMLSAQTFFGVYLVILFVLSTGSLITY 120
OY 121 FINSADPVGSSSYEDKTIPIDLVFNAAFFSFYFGLREMAADDKIKFWLEMSNVIDIETIP 180
121 finsadvpgsssyedktipidlvnafsfyfglremaaddkikfwlemsnvidietip 180
DB 121 finsadvpgsssyedktipidlvnafsfyfglremaaddkikfwlemsnvidietip 180
OY 181 PFTSYIYKSMWGLRFLRAIRLLEPOILOILAIKTSNVKSKLSTLSTWFTAG 240
181 pftsyiyksmwglrflrairllleppoilolaiiktsnvksklstlstwftag 240
DB 181 pftsyiyksmwglrflrairllleppoilolaiiktsnvksklstlstwftag 240
OY 241 FIIHVENSGDWMLKGRNSQISYFESIYLVMAWTSTVGFGVNAKTSIGRTIMEFTG 300
241 fiihvensgdwmlkgrnsqisysfesiylvmawtstvgfgvnaaktsgirtimeftg 300
DB 241 fiihvensgdwmlkgrnsqisysfesiylvmawtstvgfgvnaaktsgirtimeftg 300
OY 301 LILFANYIPEMVELFANKRKYTSYEALKGKFTVCGNITVDVTAFLRNFRLDKSGEI 360
301 lilfanyipemvelfankrkytsyealkgkftvcgnitvdvtaflrnfldrksgei 360
DB 301 lilfanyipemvelfankrkytsyealkgkftvcgnitvdvtaflrnfldrksgei 360
OY 361 NTEIYFGETPSPLELEIFKCYLAITYFISGSAMKWDLRVAVESAEALIIANPLCS 420
361 nteiyfgetpsspleleifkcylyaityfisgsamkwdlravavesaealiiannplcs 420
DB 361 nteiyfgetpsspleleifkcylyaityfisgsamkwdlravavesaealiiannplcs 420
OY 421 DSHMEDISNIRVLSIKRYDSTTRIIIOIOSHNKVYLPKIPSNMWDGDNITICPAELK 480
421 dshmedisnirvlsikrydsttriiioioshnkvylpkipsnmwdgdniticpaelk 480
DB 421 dshmedisnirvlsikrydsttriiioioshnkvylpkipsnmwdgdniticpaelk 480
OY 481 GFIAOGLVPLGCTFLSLFVEONKRVMPKOTWKHFLNSKNKILITQLSDDFAGMSFP 540
481 gfiaoglvpigctflslfveonkrvmppkotwkhflnsknkilitqlsddfagmsfp 540
DB 481 gfiaoglvpigctflslfveonkrvmppkotwkhflnsknkilitqlsddfagmsfp 540
OY 541 EVARLCFLKMWLLLAIFKSLFTDGFGLLNPPQVRIKKNLIGFIATPKDVRAL 600
541 evarlcflkmwlllaifkslftdgfgllnppqvriknknligfiatpkdvrall 600
DB 541 evarlcflkmwlllaifkslftdgfgllnppqvriknknligfiatpkdvrall 600
OY 601 FYGVCYHADVIFELITNCGCKSRROHITVPSVRMKKCLKIGSSRSRIGDSPRVSAS 660
601 fycvcyhadvifelitncgcksrrohitypsvrmmkcklkigssrsrigdspdprvsas 660
DB 601 fycvcyhadvifelitncgcksrrohitypsvrmmkcklkigssrsrigdspdprvsas 660
OY 661 TSSISNFTTRRLQHDVEDSDQLDSSGMFHWCKPTSLDKVTLKRTGSKYKFRNHIVACV 720
661 tssisnfttrrlqhdvedsdqldssgmfhwckptsldkvltlkrtskykfrnhivacv 720
DB 661 tssisnfttrrlqhdvedsdqldssgmfhwckptsldkvltlkrtskykfrnhivacv 720

DB 637 tssisnfttrtlqhdvedsdqlsdsgmfhwckptsldkvtlkrtskykfrnhivacv 696
OY 721 FGDHNSAPMGLRNVMPLRASNTRYRKLKQIVFGSLDIYQREKRFIARNPQIYILPGCA 780
721 fgdhnsapmglrnvmplrasntryrklkqivfgsldiyqrekrfiarnpqiyilpgca 780
DB 697 fgdhsapmglrnvmplrasntryrklkqivfgslidyqrewrflrnfpqiyilpgca 756
OY 781 LYSDDLAAANEOCSMKCAVLSPPQSPNSQTLVPTETAIMATLFGSLQIDSSDPPSPVS 840
781 lysddlaaanEOCSMKCAVLSPPQSPNSQTLVPTETAIMATLFGSLQIDSSDPPSPVS 840
DB 757 lysddlaaanEOCSMKCAVLSPPQSPNSQTLVPTETAIMATLFGSLQIDSSDPPSPVS 816
OY 841 EETPGYTNHNEKSNCKRVPLTELKMPNTHFTEQLGEGSLQETNLHLSTAFSTGY 900
841 eetpgytnhneksnckrvpltelkmpnthfTEQLGEGSLQETNLHLSTAFSTGY 900
DB 817 eetpgytnhneksnckrvpltelkmpnthfTEQLGEGSLQETNLHLSTAFSTGY 876
OY 901 FSSFDLSLATARYNNHVELLQMLVTGVSSQLEQHLDKKYYGADCTSLSSRN 960
901 fssfdlslatarynnhvelLQMLVTGVSSQLEQHLDKKYYGADCTSLSSRN 960
DB 877 fssfdlslatarynnhvelLQMLVTGVSSQLEQHLDKKYYGADCTSLSSRN 936
OY 961 CKLGSLSHETILSDVNPRTFQGLFCGSLDFGILCVGLYRIIDEELNPENKRFVYTR 1020
961 cklgslshetilSDVNPRTFQGLFCGSLDFGILCVGLYRIIDEELNPENKRFVYTR 1020
DB 937 cklgslshetilSDVNPRTFQGLFCGSLDFGILCVGLYRIIDEELNPENKRFVYTR 996
OY 1021 PANEFKLLPSDLVPCALPFTACYKRNDEESLQKSYEIVNKASQTEDETRHKLSSHPLI 1080
1021 panefkllpsdlvpcalpftacykRNDEESLQKSYEIVNKASQTEDETRHKLSSHPLI 1080
DB 997 panefkllpsdlvpcalpftacykRNDEESLQKSYEIVNKASQTEDETRHKLSSHPLI 1056
OY 1081 QILRHCHQSLITRSRELTSPSLFSK 1105
1081 qilrhchqslitrsreLTSPSLFSK 1105
DB 1057 qilrhchqslitrsreLTSPSLFSK 1081

RESULT 3

AAY13437
ID AAY13437 standard; Protein: 1112 AA.

XX AAY13437:

DT 26-JUL-1999 (first entry)

XX Mouse S103 (mS103).

XX Voltage-gated; pH sensitive; potassium channel; S103; spermatocyte; sperm capacitation; acrosome reaction; fertilization; infertility; XX contractile; sperm physiology; channel protein; gene therapy.

OS Mus sp.

XX WO9920754-A1.

XX PD 29-APR-1999.

XX PF 21-OCT-1998; 98WO-US22321.

XX PR 27-FEB-1998; 98US-0076172.

XX PR 22-OCT-1997; 97US-0063138.

XX PA (UNIV) UNIV WASHINGTON.

XX PI Salzkof L, Schreiber M, Silvia C;

XX DR WPI: 1999-326593/27.

XX DR N-PSDB; AAX5514.

XX PT Voltage-gated, pH-sensitive potassium channel useful in gene therapy

XX PS Claim 1; Page 77; 93pp; English.

CC The invention relates to a voltage-gated, pH sensitive potassium channel CC S103, expressed in spermatoocytes. S103 has, as a monomer, calculated CC molecular weight 120-156 kD, has unit conductance (as a functional CC tetramer, when expressed in *Xenopus* oocytes) of 80-120 pS; has increased CC activity at intracellular pH above about 7.1 and binds specifically to CC polyclonal antibodies against sequences shown in AAY13437, AAY13438,

Query Match	Best Local Similarity	Matches	Conservative	Mismatches	Indels	Gaps
65.0%	Score 3717.5;	DB 20;	Length 1112;			
69.0%;	Pred. No. 0;					
119;	Mismatches 190;	Indels 19;	Gaps 5			
1	MEOTLRNETWEDDLKMSCTPEIOAFLISSVTFPSSGLILILPRILMRSVKMQOING	60				
1	msqtlldslngkelcetacteliegaafllsslatffgallliffialksrswmyvng	60				
61	TGILLETSGTIAHSVHRSLEHOGOFRDHIEMLSAOTFVGQVILVFLVSLGSLIY	120				
61	prgllelfsrrleeanprklyfhgvtfrqiemlllsacqvvgvayllylvflslgslvay	120				
121	FINSADPVGSGSSYEDKTIPIDLVNAFPSPFFGLRPMADDKIKIKWLEMSNIVDIPTIP	180				
121	finsmdpyrcrccsyedklyvhgslfnafsfyfglyrfwaadklykfwlmsnsvldiflip	180				
181	PTFISYUUKSNMLGRLPRALRLLELPOLILRAIKTSNSVSKSLIILISTWTPTAG	240				
181	ptfisyylksnmlygrlfrtalrllelprkllqlyvaksnsyklslslvlsvcwflaag	240				
241	FHLHENSQDPLMKGRNSONISYFESSIYLVMATTSVGVGDVAAKSLSRTEFIMPTLLS	300				
241	fhlyvengsdplmgngmsqumyfeslylvatbstvsgfdgvaktslygrlfvftflgs	300				
301	LILFANTYPRWELFANKRKKTYSSTFEALKKGFYIVCGNIIVDSYATFLRNLROKSGEI	360				
301	lilfanyipremwelfstcrkkytkyreaavgkfflvvcgnllvdsvyaflnflhwksgel	360				
361	NTEIVFGETPRSLLELTFKCYLAUTTFPFISSAKMKMEDLRVAVASACILIANPLCS	420				
361	nleivfgetlprclelecllckhtscstlvgtalkfcdkrlvaveenseacillanhfcs	420				
421	DSHAEIDINIMKVLISIKNVDSFTRIILIOLOHNNKYUFLKRPISMMNDTDNIICFALKL	480				
421	dshaednslnmravlslkhyupgtvrlldlgsgnkvlflsklpwksasgdnllcfelkl	480				
481	GFIAOGCLVPGCLCTFLTSLVEQONKKVMPKQTKWKNHFLSMKNKILITQRISDDFAGMSFP	540				
481	gfiaegclvpgclctflctflleqnglvprkhpwqkfhnglknkllltqrlndfvmgtmr	540				
541	EVARLCFLKMYLLILATIEYKSLFTPGFCGLILNPRQVARIKKNITLGAFIAERPKDVRRL	600				
541	qvarlctvklmlmlalqhkprft-hsccelllnpsqvlnldctlgflfadsakvarkaf	599				
601	FYCSVGHQDVFIPELITLTCGCKSRSRONITVPSYKMKKSLGKISIRISGOOSPSPVVAS	660				
600	fycsvchqdvcmpeilgckcnckikxergqlleptlmwkslclctf-----sshlnams	654				
661	T-----SSISNFTTRTLADHVEQDSDOLDSGFMHWCCKPTSLDKVTLKRTKSGK	709				
655	teihctfcregpalitlttnprctndvddtdmlsdsgmfhwccrampldyklorekflrn	714				
710	YKFRHHYACVFGDHAAPMGRLNFWMPRLASNYTRKELKDVIFFGSLDYLQREKFRFLRN	769				

Db	715	hefgnhlvcevfqdaqctlvglrnfvmprlraasnytrqelkdvlvfgslsleyfgdrewflrn	774		
Qy	770	FPQIYIIPGCAIYSGDLHAANIQCSCMAVSPPOSSNQTLVDTIATMTLTGSLQI	829		
Db	775	fpkhhmpgslaylmgdliavnevcsmcvllatprykalsqdlvdtcaalmalnqslrli	834		
Qy	830	DSSSDPSPSVSEETPGYT -GNHNEKSNCKRKVRPLTEPLKMPNSNHFEOLGEGESLOETN	888		
Db	835	-tscptgssskvexkpsaafskerkqgrvyqjrlpilletkmpsnhltedmgglidgmhkgts	893		
Qy	889	LHUSTATSTGVSSSPFLSDSLATAFYNNHVELLOMLVTGCVSSQLEQHLDPKDVVGYVA	948		
Db	894	lhststsgtavgadrtldslatlsfynhvvelqlmlyvtgglassemeelylvekprytc	953		
Qy	949	DGCTSLISGRNCKLGLSLHEFTILSDVNPRTFGOLFCSLDLFGILCVGLYRIIDEE	1008		
Db	954	dgyeakrctrcrkglisldqvtlsgltnprkfgqlfcgsldnfgllvcvgyrmdidee	1013		
Qy	1009	LNPENKRFVITRANPEKFLPSLVCAIPESACK	1045		
Db	1014	psgehkrviltprsnecghlpsdlvtcaipfnltcgk	1050		
RESULT 4					
ID	AA132017	AA132017 standard; Protein; 1196 AA.			
XX	AA132017:				
AC	AA132017:				
DT	05-JAN-2000	(first entry)			
DE	Mouse cation channel protein.				
XX					
KW	Cation channel protein; CCP, ion transport; arrhythmia;				
KM	diabetes mellitus; seizure; asthma; hypertension; therapy;				
KW	protein engineering; mouse.				
XX					
OS	Mus musculus.				
XX					
XX					
FT	Key	Location/Qualifiers			
FT	Region	61..119			
FT		/note="Crystal region"			
XX	W09947923-A2.				
XX					
PD	23-SEP-1999.				
XX					
PF	22-MAR-1999;	99MO-US06307.			
XX					
PR	20-MAR-1998;	98US-0045529.			
PR	02-APR-1998;	98US-0054347.			
XX					
PA	(UYRQ) UNIV ROCKEFELLER.				
XX					
PI	MacKinnon R;				
XX					
DR	WPI; 1999-601131/51.				
XX					
PT	Assays for screening compounds which interact with cation channel				
PT	proteins; useful for providing agents for treatment of diseases -				
XX					
PS	Claim 21; Page 144-147; 165pp; English.				
XX					
CC	The present sequence represents an assay cation channel protein				
CC	(CCP). The invention provides an assay for screening potential				
CC	drugs or agents which interact with CCPs using prokaryotic CCPs				
CC	(such as those given in AA132009-12) mutated, using recombinant DNA				
CC	technology, to mimic the physiological function and chemical				
CC	properties of a functional eukaryotic CCP (such as those given in				
CC	AA132013-22). An example of a mutated prokaryotic CCP is given in				
CC	AA132024. The crystal region of the CCP may also be used in the				
CC	assay. The drugs or agents obtained can be used to treat				
CC	conditions related to the function of CCP in vivo, such as cardiac				

XX Cation channel protein; CCP; ion transport; arrhythmia;
 KW diabetes mellitus; seizure; asthma; hypertension; therapy;
 KW protein engineering; human.

OS Homo sapiens.

XX Key Location/Qualifiers
 FH Region 61..119
 FT /note="crystal region"

XX MO9947923-A2.

XX 23-SEP-1999.

XX 22-MAR-1999; 99MO-US06307.

XX 20-MAR-1998; 98US-0045529.

XX 02-APR-1998; 98US-0054347.

XX (UNIQ) UNIV ROCKEFELLER.

XX Mackinnon R;

XX WPI; 1999-601131/51.

PT Assays for screening compounds which interact with cation channel
 PT proteins, useful for providing agents for treatment of diseases -
 PS Claim 21; Page 137-140; 165pp; English.

XX The present sequence represents a human cation channel protein
 CC (CCP). The invention provides an assay for screening potential
 CC drugs or agents which interact with CCPs using prokaryotic CCPs
 CC (such as those given in AAY32009-12) mutated, using recombinant DNA
 CC technology, to mimic the physiological function and chemical
 CC properties of a functional eukaryotic CCP (such as those given in
 CC AAY32013-22). An example of a mutated prokaryotic CCP is given in
 CC AAY32024. The crystal region of the CCP may also be used in the
 CC assay. The drugs or agents obtained can be used to treat
 CC conditions related to the function of CCP in vivo, such as cardiac
 CC arrhythmia, diabetes mellitus, seizure disorder, asthma or
 CC hypertension. The invention has overcome the physical limitations
 CC regarding the isolation and purification of eukaryotic CCPs.

XX Sequence 858 AA:

Query Match 2.8%; Score 158.5; DB 20; Length 858;
 Best Local Similarity 22.6%; Pred. No. 6.1e-06;
 Matches 65; Conservative 64; Mismatches 123; Indels 35; Gaps 8;

QY 103 QVLVLVLSIGSLIIFINSADPVSGSCSYEDKT-----IPIDLVENAFSEFYGLRF 157
 DB 189 KILALISLIFVLSLSTSLINLDELGLDELGSGTDPQLAHVAEVCRAWFTMEYLLIRF 248
 QY 158 MAADDKIKFMLEMNSIVDIFTPFTFISVYL-KSNMVLGRFARLRLELPQILQLRAI 216
 DB 249 ISPPKKWKFIFGPNALIDIALIPYVCLFLESNKSVIQGNVTRVQILIRIMILLI 308
 QY 217 KTSNSVKESKLSILSTWFTAGFIHLVENSQDPWLK-----GRNSONISYFESI----- 267
 DB 309 KLARHSGLSIGLFTIRSYNELGILLIFLMDGLMIFSLVFAEKDEDDKFKSLPSAF 368
 QY 268 YLVMAITTSVGERGVNATSLGRTIFMTGLSLLFPANVIREMVELR-----NKRK 320
 DB 369 WWTLMFTVYGDLYPTLLIGKIVGGLCAGVLAIPILVYNNISSEFYKQKRGK 428
 QY 321 YTSYEALGKKFIYVCGN---ITVDSYTAFLR-----NFLRDKSGE 359
 DB 429 ATRKREALERAK-----TNGSLVMMKDAFERSLEMDIVVEKNGE 470

RESULT 12

AAAY44565
 ID AAY44565 standard; Protein: 519 AA.

XX AAY44565;

XX 04-APR-2000 (first entry)

XX Human Voltage-gated Potassium channel monomer, Kv6.2 polypeptide.

XX Voltage gated potassium channel; Kv6.2; human; excitability; ion flux;
 KW resting potential; alpha subunit; modulator; hearing/vision problem;
 KW migraine; central nervous system; CNS; seizure; neuroprotective agent;
 KW psychotic disorder; reporter; treatment; detection; antibody; probe;
 KW primer.

XX Homo sapiens.

XX Key Location/Qualifiers
 FH Misc-difference 463..465
 FT /note="This region of the protein sequence is
 FT represented in the specification by the typographical
 FT error Kv6.2 which is an insertion of the protein name"

XX WO200001811-A1.

XX 13-JAN-2000.

XX 30-JUN-1999; 99MO-US14945.

XX 01-JUL-1998; 98US-0091466.

XX (ICAG-) ICAGEN INC.

XX Jegla TJ;

XX WPI; 2000-126937/11.

XX N-PSDB; AAZ49455.

XX New voltage-gated potassium channel alpha subunit, useful for
 PT identifying modulators of voltage-gated channel activity useful for
 PT treating central nervous system disorders e.g. migraines and as
 PT neuroprotective agents -

XX Claim 14; Page 66; 80pp; English.

XX The present amino acid sequence is the human Kv6.2 monomer, which is an
 CC alpha subunit of a heteromeric voltage-gated potassium channel. It is
 CC isolated from brain tissue and maintains the resting potential and
 CC controls the excitability of a cell. Kv6.2 polypeptide can be used to
 CC identify compounds, that modulate the ion flux through heteromeric
 CC voltage-gated potassium channels. Such modulators are used as
 CC neuroprotective agents and for treating CNS disorders, such as migraines,
 CC hearing and vision problems, psychotic disorders and seizures. It can
 CC be used as reporter molecules in assays and to produce antibodies.
 CC Kv6.2 DNA sequence can be used to produce specific primers or probes
 CC for detection purposes.

XX Sequence 519 AA:

Query Match 2.7%; Score 154.5; DB 21; Length 519;
 Best Local Similarity 22.8%; Pred. No. 6.3e-06;
 Matches 64; Conservative 50; Mismatches 108; Indels 59; Gaps 6;

QY 122 INSADPVSGSCSYEDKTIPIDLVENAFSEFYGLRFMAADDKIKKMLEMNSIVDIFTPP 181
 DB 246 LRAEEDGECSTKCYIFIVETLCVAFSLFELCFVGAQDCGFQGPLNIDILALSP 305
 QY 162 TFIISY-----YLSKNMVLGRFARLRLELPQI-----QLIRAKT 218
 DB 306 YVSVLAVSEEPDEGERPSRYSYLEKVGIVIRVIRALIRIYVMILARHSLGIGLIVR 365

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 7, 2001, 09:43:27 ; Search time 9921.66 Seconds
(without alignments)
3162.175 Million cell updates/sec

Title: US-09-176-664-17

Perfect score: 3319

Sequence: 1 atgttcagactaagctacg.....tctttcctaagaacaatag 3319

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 10228115 seqs, 4726426750 residues

Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Db 364 ACTTATATGACAGATGCGGACATGATGGAATGCTCAAAAGGACTACGTTGCATCTCA 423
Qy 2675 gcaatgaccttcttaacggagcaatgtttctccagcaagctcttgatctctgctgcca 2734
Db 424 GCACCTCTTCTCCACGCGGAGTGTCTTTTCAGACACCTTCTTGGAATCTCTCTCGGCCA 483
Qy 2735 cggcctcttaacattatcatatgctccgtgaattgcttcagatgctggtgacagaggaata 2794
Db 484 CGTCTTCTTCAATTAACAGATGCTGTGAATTAATTAATTAATTAATTAATTAATTAATTA 543
Qy 2795 gttccagcagacaacatagataagataaagctatgg 2837
Db 544 GCCTGTGATGAGAACACTATTGTGTTAAGAGAGAACCCCTATAG 586

RESULT 2
LOCUS BE012861 524 bp mRNA EST 09-JUL-2000
DEFINITION 122576 MARC 1p16g Sus scrofa cDNA 5', mRNA sequence.
ACCESSION BE012861
VERSION BE012861.1 GI:8273800
KEYWORDS EST.
SOURCE Sus scrofa
ORGANISM pig.

REFERENCE 1 (bases 1 to 524)
AUTHORS Mammalia: Eutheria; Cetartiodactyla; Suidae; Sus.
Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E.,
Stone, R.T., Heaton, M.P., Grose, W.M., Bennett, G.A., Laegreid, W.W.,
and Keele, J.W.
Design and use of two pooled tissue normalized cDNA libraries for
EST discovery in swine

TITLE EST discovery in swine
JOURNAL Unpublished (2000)
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@mail.marc.usda.gov
Single pass sequencing. Bases called and alt-trimmed with phred
v0.980904.e. Vector identified by cross_match with the -mnscore 18
and -mismatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCACAGTACAGCAGC
Plate: 46 row: B column: 16
Seq primer: ATTAGGTGACACTATAG.
Location/Qualifiers

FEATURES
source
1..524
/organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC 1p16g"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled tissue from day 11, 13, 15, 20,
and 30 embryos."

BASE COUNT 132 a 119 c 134 g 139 t
ORIGIN

Query Match 7.0%; Score 233.2; DB 162; Length 524;
Best Local Similarity 80.1%; Pred. No. 3.4e-55;
Matches 301; Conservative 0; Mismatches 68; Indels 7; Gaps 2;

Qy 1977 aagcacttgagagatcaaacctccaccagagctcttcaacagatgtagaacaaga 2036
Db 155 ACACACTGTGCTCATAGTCCAGAGACATTCAGCGCTTTCACTATGAAATGGAACAA-- 212
Qy 2037 ttctgacagcttgatagcagatgtagatgttctacgtgtgcaaaccaacctcttgacaa 2096
Db 213 ----GACACCTTGATTAACACTGGCATGTTTCTGCTGTGACAGAGCCACCCATTGGACAA 268

Qy 2097 ggtgactctgaaacgaactggaagtcgaagataaagttcggaaacataatgtagcatg 2156
Db 269 AATGATTCCTGAAGAAAGAACTGACAAAGTCAAAGATGTTGGGAACCATCGTGCATG 328
Qy 2157 tggatatt-ggaagatgcccactcagcccgatggggtcttggaactttgataagccctga 2215
Db 329 TGTCTTTGGAGATGCCCATTCGACCTGTGAGGGGCTTCGAAATTTGTAATCCACTGA 388
Qy 2216 gaagcagacactataccagaagaagagcgtgaagacatagttcatatggctcctgagct 2275
Db 389 GACCTAGCAACTACACCCGCAAGAGCTGAAGACATTTGTTGGGTCTCTGGATT 448
Qy 2276 atctacagagaagaatggagatcttccggaatttcccaacatatacatctgctgagat 2335
Db 449 ACCTGACAGAGAGATGGCATTCCTCGGAATTTCCCGAGATATATTCTTCTCGATG 508
Qy 2336 gtgcacttaattctgg 2351
Db 509 CTGCGCTCTATTCTGG 524

RESULT 3
LOCUS A0477745 652 bp DNA GSS 23-APR-1999
DEFINITION CITR1-E1-2591F7.TF CITR1-E1 Homo sapiens genomic clone 2591F7,
sequence.
ACCESSION A0477745
VERSION A0477745.1 GI:4659864
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 652)
AUTHORS Mammalia: Eutheria; Primates; Catarrhini; Homnidae; Homo.
Zhao, S., Adams, M.D., Nierman, W., Malek, J., Shizuya, H., Simon, M. and
Venter, J.C.
End Sequences from Caltech Libraries for Sequence-Ready
Map Building
Unpublished (1997)
COMMENT Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbe@tigr.org
Clones are available from Research Genetics (Info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/hungen/bac_end_search/bac_end_search.html.
Seq primer: M13-21
Class: BAC ends.
Location/Qualifiers

FEATURES
source
1..652
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="2591F7"
/clone_lib="CITR1-E1"
/sex="male"
/cell_type="sperm"
/note="Vector: pBelobAC11; Site_1: EcoRI; Site_2: EcoRI;
Caltech Human BAC Library D"

BASE COUNT 198 a 165 c 122 g 167 t
ORIGIN

Query Match 6.9%; Score 227.4; DB 229; Length 652;
Best Local Similarity 98.8%; Pred. No. 1.7e-53;
Matches 250; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

Qy 3041 aagagcttgatcacccggcagcaatgagttcaagctgctgcttcagatctgtgt 3100
Db 402 ACAGTTTGTGATCACCCGCGCAGCCCAATGATTAAGTCTGCTTCAGATCTTGTGT 461

Query Match	6.6%	Score 219;	DB 189;	Length 329;
-------------	------	------------	---------	-------------

[illegible]

	LOCUS	A1129381/c	509 bp	mRNA	EST	27-OCT-1998
	DEFINITION	gc34d02.x1 Soares_pregnant_uterus_Nbhpu Homo sapiens cDNA clone IMAGE:1711491 3' similar to TR:Q12791 Q12791 CALCIUM-ACTIVATED POTASSIUM CHANNEL; contains Alu repetitive element.; mRNA sequence.				
	ACCESSION	A1129381				
	VERSION	A1129381.1	GI:3597895			
	KEYWORDS	EST.				
	SOURCE	human.				
	ORGANISM	Homo sapiens				
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euarchia; Primates; Carnivora; Homnidae; Homo.				
	REFERENCE	1 (bases 1 to 509)				
	TITLE	Nci-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.				
	JOURNAL	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index				
	COMMENT	Unpublished (1997) Contact: Robert Strausberg, Ph.D. Email: cgaps@remail.nih.gov This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 699 Std Error: 0.00 Seq primer: -40m13 fwd. ET from Amersham High quality sequence stop: 444. Location/Qualifiers 1..509				
	FEATURES	/organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:1711491" /clone_lib="Soares_pregnant_uterus_Nbhpu" /sex="female" /dev_stage="adult" /lab_host="DH10B" /note="Organ: uterus; Vector: pT7/p3-Pac; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' AAGTCGAAGAATTCGGCCGCCCTTTTTTTTTTTTTTTTTT 3'] double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7/p3 vector. Library went through one round of normalization. Library constructed by M. Fatima Bonaldo."				
	BASE COUNT	131 a 108 c 118 g 152 t				
	ORIGIN					
Oy	Query Match	Best Local Similarity	4.6%;	Score 153.6;	DB 16;	Length 509;
Db	Matches 289;	Conservative	0;	Mismatches 199;	Indels	Gaps 1;
Oy	1333 atcaccatcacagatatctgcatccatccccacaaggattactgtgccaaagtctccagcttg	1392				
Db	509 ATCATCACTCAAATGTCTGCAGATTATACAAACAAGCCCATTCTCTTAACATVCCCGACTGG	450				
Oy	1393 aaactggagaccccggaagacacalcaictgcttctgtgtaatltaaactlgyatttlacggc	1452				
Db	449 AATTGGAAAAGAGGATGATGATCAGCATCTGCTCGGAGAGTGAAGTGTCGCTTCAATAGCC	390				
Oy	1453 caaagctgttgtgtgtcccaggtctgtgatccttcctaaccatccttatitgtgagccaaac	1512				
Db	389 CAGACCTCGCTGGCTCACAGGCTCTTCACACATGCTTGGCCCMACCCTTCTCCATGAGTCA	330				
Oy	1513 aaaagaagttagtcctaaacagacccggaaagaacctttttaaatgcatgaaaacaaa	1572				
Db	329 TTCAATAAGATTTGAGGAAGAACACATGGCCAGAAATACTTACTTGGAAAGAGTCTCAAAATGA	270				
Oy	1573 attctgaccaacagctctctctgtactgtactgttgcggaaatgagctllcttctgaagtgcgg	1632				
Db	269 AATGACACAGAAATATCTCTCCAGTGGCTTCGGGGGCTCTCTCCCTCACTGTTTGTAG	210				
Oy	1633 ctctgtctcttgaagatgtacctctctgtgtatagcatacgaatcaaagtccctctltag	1692				
Db	209 CTGTGTTTTTTGTAACCTCAAGCTCTCAATGATGAGCCATTGAGTACAAAGT-----TGCC	156				

QY	1693	gctgtcttcgtggtcgtcgtatctaataatcccaactcccaagaigtgaagatcgcgtaaagaacaa	1752
Db	155	AACCCAGAGAGGCCGATATTAATTAATCTGGAAACCATCTTAACATCCACAGAGGTACT	96
QY	1753	ctgaagcttcctatctgctgaactccaaagagcgtcagaagagcctgttctactgttca	1812
Db	95	TTAGCATTTTTCATGTCGCAAGTCATGTCGCAAGAGTTAAAGGCGCATTTTTTTTACTGCAAG	36
QY	1813	gtctgtcatcatga	1826
Db	35	GCCTGTCAATGATGA	22
RESULT	11		
LOCUS	A1095675/C		
DEFINITION	A1095675	507 bp	mRNA
ACCESSION	q20a12.x1	Soares_pregnant_uterus_NbHPU	Homo sapiens cDNA clone
VERSION	IMAGE:1696798.3	similar to RF:Q12791.Q12791	CALCIUM-ACTIVATED
KEYWORDS	PORASSIUM CHANNEL		mRNA sequence.
KEYWORDS	A1095675		
KEYWORDS	A1095675.1	GI:3434651	
KEYWORDS	EST.		
ORGANISM	human.		
ORGANISM	Homo sapiens		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
ORGANISM	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	1 (bases 1 to 507)		
AUTHORS	NCI-CGAP	http://www.ncbi.nlm.nih.gov/ncicgap.	
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),		
JOURNAL	Tumor Gene Index		
COMMENT	Unpublished (1997)		
COMMENT	Contact: Robert Strausberg, Ph.D.		
COMMENT	Email: cgapds-remail.nih.gov		
COMMENT	This clone is available royalty-free through LNL; contact the		
COMMENT	IMAGE Consortium (info@image.lnl.gov) for further information.		
COMMENT	Insert Length: 664 Std Error: 0.00		
COMMENT	Seq primer: -40m13 fwd. ET from Amersham		
COMMENT	High quality sequence stop: 394.		
FEATURES	Location/Qualifiers.		
source	1..507		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	/clone="IMAGE:1696798"		
	/clone_lib="Soares_pregnant_uterus_NbHPU"		
	/sex="female"		
	/dev_stage="adult"		
	/lab_host="DH10B"		
	/note="Organ: uterus; Vector: pT7n3-Pac; Site:1: Not I;		
	Site:2: Eco RI; 1st strand cDNA was primed with a Not I -		
	oligo(dt) primer [5,		
	AACGcAGAGAAATTCGGCGCGCCCTTTTTTTTTTTTTTTTTTTT 3'],		
	double-stranded cDNA was ligated to Eco RI adaptors		
	(Pharmacia), digested with Not I and cloned into the Not I		
	and Eco RI sites of the modified pT7n3 vector. Library		
	went through one round of normalization. Library		
	constructed by M. Fatima Bernaldo."		
BASE COUNT	133 a 109 c 116 g 148 t	1 others	
ORIGIN			
Query Match	4.5%	Score 149.2;	DB 16; Length 507;
Best Local Similarity	57.7%	Pred. No. 3.4e-31;	
Matches	287; Conservative	0; Mismatches 204;	Indels 6; Gaps 1.
QY	1330	agatcatcatatcagatctgcatccccaatacaagttatctgcccagaagatctccagc	1389
Db	504	AGCATCATCATCAATTCGTCGAGTATACANNAAGGCCCATCTGCTAACAATCCGAGC	445
QY	1390	tggaaatggaaagaggtgatgacgcatctccgcgacagattgaaagttggcgttcata	385
Db	444	TGGAATTTGAAAGAGGTGATGATGACGATTCCTCCGCGACAGATTGAAATTTGGCGTTCA	385

Db 90 ACCTTAGGATTTTTCATCCCAAGTAGTCGCAAGAAGTTACAGAGGCATTTTTCCTGC 31
 QY 1810 tcagtcctcatgatga 1826
 Db 30 AAGGCTGTGATGATGA 14

RESULT	15
AA072586	
LOCUS	377 bp mRNA
DEFINITION	Stratagene mouse macrophage (J937306) Mus musculus cDNA

BASE COUNT	112 a	96 c	85 g	83 t	1 others
ORIGIN					

Query Match	3.9%	Score 128.2	DB 2	Length 377
Best Local Similarity	77.1%	Pred. No. 3.1e-25		
Matches 168	0	Mismatches 49	Indels 1	Gaps 1

[illegible]

Db	279	AGAACCCACATTTGTAGTATGCCGTGTTTGAGACATGCCCAATGTACCCCTGCTGGGCTTCGGA	338
Qy	2198	actctgttaatgcctctgagagccgaactataaccag	2235
Db	339	ATTTCGTGATGCCCTCGAGACCCAGCAATCACACCCGG	376

Search completed: October 7, 2001, 09:43:57
Job time: 20598 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 7, 2001, 09:50:45 ; Search time 244.36 Seconds
(without alignments)
2571.303 Million cell updates/sec

Title: US-09-176-664-17

Perfect score: 3319
Sequence: 1 atgttcagactaagctacg.....tcttctcctaagaatag 3319

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 324599 seqs, 9465562 residues

Total number of hits satisfying chosen parameters: 649198

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: Issued_Patents_NA.*
2: /cgn1_7/ptodata/1/lna/5A-COMB.seq.*
3: /cgn1_7/ptodata/1/lna/5B-COMB.seq.*
4: /cgn1_7/ptodata/1/lna/6A-COMB.seq.*
5: /cgn1_7/ptodata/1/lna/6B-COMB.seq.*
6: /cgn1_7/ptodata/1/lna/6C-COMB.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	57.4	1.7	311	3	US-09-035-648-6
2	57.4	1.7	311	4	US-09-001-951-6
3	36.6	1.1	7218	1	US-08-232-463-14
4	35.4	1.1	2876	4	US-09-134-607A-9
5	35.4	1.1	2876	4	US-09-134-607A-14
6	33.8	1.0	1306	4	US-09-387-574-3
7	33.6	1.0	1518	2	US-08-929-501-4
8	33.6	1.0	1518	2	US-08-929-501-5
9	33.6	1.0	1518	3	US-09-140-177-4
10	33.6	1.0	1518	3	US-09-140-177-5
11	33.6	1.0	1518	4	US-09-397-979-4
12	33.6	1.0	1518	4	US-09-397-979-5
13	33.6	1.0	1753	2	US-08-929-501-1
14	33.6	1.0	1753	2	US-08-929-501-3
15	33.6	1.0	1753	3	US-09-140-177-1
16	33.6	1.0	1753	3	US-09-140-177-3
17	33.6	1.0	1753	4	US-09-397-979-1
18	33.6	1.0	1753	4	US-09-397-979-3
19	33.6	1.0	1770	2	US-08-929-501-11
20	33.6	1.0	1770	2	US-08-929-501-13
21	33.6	1.0	1770	3	US-09-140-177-11
22	33.6	1.0	1770	3	US-09-140-177-13
23	33.6	1.0	1770	4	US-09-397-979-11
24	33.6	1.0	1770	4	US-09-397-979-13
25	33.6	1.0	2073	2	US-08-929-501-25
26	33.6	1.0	2073	3	US-08-929-501-26
27	33.6	1.0	2073	3	US-09-140-177-25

c	28	33.6	1.0	2073	3	US-09-140-177-26	Sequence 26, Appl
c	29	33.6	1.0	2073	4	US-09-397-979-25	Sequence 25, Appl
c	30	33.6	1.0	2073	4	US-09-397-979-26	Sequence 26, Appl
c	31	33	1.0	751	4	US-08-998-416-1084	Sequence 1084, Ap
c	32	33	1.0	751	4	US-09-130-242-7	Sequence 7, Appl
c	33	33	1.0	2121	2	US-08-897-340-6	Sequence 6, Appl
c	34	33	1.0	2121	3	US-09-252-329-6	Sequence 6, Appl
c	35	33	1.0	3773	4	US-09-130-242-1	Sequence 21, Appl
c	36	32.8	1.0	1025	2	US-08-482-728A-20	Sequence 20, Appl
c	37	32.8	1.0	1122	2	US-08-482-728A-21	Sequence 21, Appl
c	38	32.8	1.0	1230	4	US-09-387-574-5	Sequence 5, Appl
c	39	32.8	1.0	1248	2	US-08-897-340-5	Sequence 5, Appl
c	40	32.8	1.0	1248	3	US-09-252-329-5	Sequence 5, Appl
c	41	32.8	1.0	1424	2	US-08-915-972A-21	Sequence 21, Appl
c	42	32.8	1.0	1424	2	US-09-177-909-21	Sequence 21, Appl
c	43	32.8	1.0	2173	1	US-08-795-788-1	Sequence 1, Appl
c	44	32.8	1.0	2173	5	PCT-US93-03942-1	Sequence 1, Appl
c	45	32.8	1.0	2799	1	US-08-212-188-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-09-035-648-6
Sequence 6, Application US/09035648
Patent No. 6100031
GENERAL INFORMATION:
APPLICANT: Shyjan, Andrew W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
DIAGNOSIS, PREVENTION, AND TREATMENT OF NEOPLASTIC CELL
TITLE OF INVENTION: GROWTH AND PROLIFERATION
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/035, 648
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/818, 829
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Melkijohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/003001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 311 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-09-035-648-6
Query Match 1.7%, Score 57.4, DB 3, Length 311;
Best Local Similarity 59.5%, Pred. No. 4.3e+08;
Matches 97, Conservative 0, Mismatches 66, Indels 0, Gaps 0;

Oy 460 ggaatgagttatgacgcctgatacagaatcaagttctgctgagatgaattcaalc 519
Db 1268 yyy 1327
Oy 520 gtagacatcttacacccacacacatttcttatttgaagaagcaattgacta 579
Db 1328 yyy 1387
Oy 580 gglttaagttccctcaagagcctgctgctgacgaactccctcaaatcttgcaattcta 639
Db 1388 yyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyyygtagccaaattctt 1447
Oy 640 cgaagc 644
Db 1448 ctatc 1452

RESULT 4
US-09-134-607A-9
; Sequence 9, Application US/09134607A
; Patent No. 6252141
; GENERAL INFORMATION:
; APPLICANT: Joseph Hirschberg et al.
; TITLE OF INVENTION: POLYNUCLEOTIDES CONTROLLING THE EXPRESSION
; TITLE OF INVENTION: OF AND CODING FOR GENE B IN TOMATO AND USE
; TITLE OF INVENTION: OF SAME FOR ALTERING CAROTENOID
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
; STREET: 20001 Jefferson Davis Highway, Suite 207
; CITY: Arlington
; STATE: Virginia
; COUNTRY: United States of America
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
; COMPUTER: Twinhead, Slimnote 8907x
; OPERATING SYSTEM: MS DOS version 6.2,
; OPERATING SYSTEM: Windows version 3.11
; SOFTWARE: Word for Windows version 2.0,
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/134,607A
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Friedman, Mark M.
; REGISTRATION NUMBER: 33,883
; REFERENCE/DOCKET NUMBER: 325/12
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 972-3-562553
; TELEFAX: 972-3-562554
; TELEX:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2876
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-09-134-607A-9

Query Match 1.1%, Score 35.4; DB 4; Length 2876;
Best Local Similarity 54.1%; Pred. No. 1.5;
Matches 72; Conservative 0; Mismatches 61; Indels 0; Gaps 0;
Oy 1967 gggatctgcgaagcacttcagacatacaacttaccacccagagctcttcaacatgag 2026
Db 665 GGTAATATATAACCTTTTCTTTATGAGAAAGTTCACCGAATATATTTCTATTGTGG 724

Oy 2027 tagacaagatttcaccagcttgatagcagtg99gatgttcaactggtgcacaaccact 2086
Db 725 CATATATAGTATAGTGCAGATTGACAGAAATTATTTTGCAGTTGGGCACATGAAACA 784
Oy 2087 ctltggacaagt 2099
Db 785 TTTTCCTCAAGT 797

RESULT 5
US-09-134-607A-14
; Sequence 14, Application US/09134607A
; Patent No. 6252141
; GENERAL INFORMATION:
; APPLICANT: Joseph Hirschberg et al.
; TITLE OF INVENTION: POLYNUCLEOTIDES CONTROLLING THE EXPRESSION
; TITLE OF INVENTION: OF AND CODING FOR GENE B IN TOMATO AND USE
; TITLE OF INVENTION: OF SAME FOR ALTERING CAROTENOID
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
; STREET: 20001 Jefferson Davis Highway, Suite 207
; CITY: Arlington
; STATE: Virginia
; COUNTRY: United States of America
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
; COMPUTER: Twinhead, Slimnote 8907x
; OPERATING SYSTEM: MS DOS version 6.2,
; OPERATING SYSTEM: Windows version 3.11
; SOFTWARE: Word for Windows version 2.0,
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/134,607A
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Friedman, Mark M.
; REGISTRATION NUMBER: 33,883
; REFERENCE/DOCKET NUMBER: 325/12
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 972-3-562553
; TELEFAX: 972-3-562554
; TELEX:
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2876
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-09-134-607A-14

Query Match 1.1%, Score 35.4; DB 4; Length 2876;
Best Local Similarity 54.1%; Pred. No. 1.5;
Matches 72; Conservative 0; Mismatches 61; Indels 0; Gaps 0;
Oy 1967 gggatctgcgaagcacttcagacatacaacttaccacccagagctcttcaacatgag 2026
Db 665 GGTAATATATAACCTTTTCTTTATGAGAAAGTTCACCGAATATATTTCTATTGTGG 724
Oy 2027 tagacaagatttcaccagcttgatagcagtg99gatgttcaactggtgcacaaccact 2086
Db 725 CATATATAGTATAGTGCAGATTGACAGAAATTATTTTGCAGTTGGGCACATGAAACA 784
Oy 2087 ctltggacaagt 2099
Db 785 TTTTCCTCAAGT 797


```

ADDRESS: Carol Talkington Verser, Ph.D.
ADDRESSEE: Heska Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Wordperfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/929,501
FILING DATE: 15-SEP-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: HM-6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1753 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-929-501-3

Query Match
Best Local Similarity 1.0%; Score 33.6; DB 2; Length 1753;
Matches 75; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 2776 ctgtgacagagagagtaagttctcagctggaacaacattagataagataagtcatt 2835
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 655 CTGTGACCAACCAAGGCTGTTGATCTTCATCTGAGAGATCAATGGAGATGAGAAATCCCTCGTA 596

QY 2836 ggtgttgagagatagctgacgtcgtctctgtctggaagaacccggtgtgaagcttggtc 2895
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 595 AGTCACAGTAAAAAGAAATAAGATCTTAATTGAACCTTTCGCATCTGCACAGGCGCAGTG 536

QY 2896 ctgtcctaccacgaacacattta 2919
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 535 CTTTCATTAATTTCACGCAGATTa 512

RESULT 15
US-09-140-177-1
: Sequence 1, Application US/09140177
: Patent No. 6042825
: GENERAL INFORMATION:
: APPLICANT: Ramaswamy Chandrashekar
: APPLICANT: Naotoshi Tsuji,
: TITLE OF INVENTION: PARASITIC HELMINTH ASPARAGINASE
: TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES, AND
: TITLE OF INVENTION: USES THEREOF
: NUMBER OF SEQUENCES: 26
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Carol Talkington Verser, Ph.D.
: ADDRESS: Heska Corporation
: STREET: 1825 Sharp Point Drive
: CITY: Fort Collins
: STATE: Colorado
: COUNTRY: USA
: ZIP: 80525
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: Windows 95

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 7, 2001, 19:18:11 ; Search time 733.38 Seconds
(without alignments)
2841.645 Million cell updates/sec

Title: US-09-176-664-17

Perfect score: 3319
Sequence: 1 atgttcagactaagctacg.....tctttcctaagcaatag 3319

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues

Total number of hits satisfying chosen parameters: 1460202

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_0601:*

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22: /cgnl_9/gcgdata/geneseq/geneseqn/NA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	3318.6	100.0	3319	AAK55524
2	3163.6	95.3	3247	AAK55525
3	1857	56.0	3339	AAK55514
4	376	11.3	416	AAK55515
5	94.4	2.8	936	AAK58252
6	94.4	2.8	936	AAK58254
7	94.4	2.8	936	AAK58257
8	94.4	2.8	936	AAK58259
9	94.4	2.8	936	AAK58262
10	94.4	2.8	938	AAK58255
11	93.4	2.8	936	AAK58252

12	93.4	2.8	936	22	AAK58254	Oligonucleotide D1
13	93.4	2.8	936	22	AAK58257	Oligonucleotide D1
14	93.4	2.8	936	22	AAK58259	Oligonucleotide D2
15	93.4	2.8	936	22	AAK58262	Oligonucleotide D2
16	93.4	2.8	938	22	AAK58255	Oligonucleotide D1
17	57.4	1.7	311	18	AAK91705	Gene 056 fragment
18	41.6	1.3	244	20	AAK58238	Oligonucleotide D1
19	41.6	1.3	1887	22	AAK58238	Enterococcus faec
20	41	1.2	244	22	AAK58238	Enterococcus faec
21	40	1.2	580073	18	AAK58840	Oligonucleotide D1
22	38.4	1.2	1866	20	AAK59653	Mycoplasma genital
23	37.4	1.1	6531	20	AAK13012	Nucleic acid sequ
24	36.8	1.1	1449	18	AAK72643	Enterococcus faec
25	36.6	1.1	1549	21	AAK16638	Human calpastatin
26	36.6	1.1	2919	21	AAK38526	Human secreted pro
27	36	1.1	49998	20	AAK33518	CDNA encoding Euc
28	35.6	1.1	2701	20	AAK6143	Human Kidney amino
29	35.4	1.1	2876	20	AAK6143	DNA encoding a pot
30	35.4	1.1	16941	21	AAK234737	L. esculentum lyco
31	35	1.1	9828	19	AAK52174	Drosophila disaetl
32	34.6	1.0	1331	21	AAK33370	Streptococcus pneu
33	34.4	1.0	767	20	AAK16218	Human secreted pro
34	34.4	1.0	1206	17	AAK09352	Human gene express
35	34.2	1.0	1995	19	AAK53550	Aureobasidin resis
36	34.2	1.0	3451	18	AAK02308	DNA encoding a ace
37	34.2	1.0	7481	18	AAK4547	Cell membrane prot
38	34.2	1.0	9326	21	AAK51236	Staphylococcus aur
39	34.2	1.0	17310	18	AAK4334	Staphylococcus aur
40	34	1.0	300	20	AAK12908	Human gene express
41	34	1.0	789	20	AAK15761	Human gene express
42	34	1.0	789	20	AAK15762	Human gene express
43	33.8	1.0	1306	22	AAK91092	Human gene express
44	33.8	1.0	1401	21	AAK00096	Soybean geranylger
45	33.8	1.0	1729	10	AAK91686	Human zsl99 degen

ALIGNMENTS

RESULT 1	
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ID	AAK55524:
AC	AAK55524:
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DT	26-JUL-1999 (first entry)
XX	
DE	Nucleotide sequence of hsl03-1.
XX	
KW	Voltage-gated, pH sensitive; potassium channel; S103; spermatocyte;
KW	sperm capacitation; acrosome reaction; fertilization; infertility;
KW	contraceptive; sperm physiology; channel protein; gene therapy; ss.
XX	
OS	Homo sapiens.
XX	
PN	W09920754-A1.
XX	
PD	29-APR-1999.
XX	
PF	21-OCT-1998; 98WO-US22321.
XX	
PR	27-FEB-1998; 98US-0076172.
XX	
PR	22-OCT-1997; 97US-0063138.
XX	
PA	(UNIV) UNIV WASHINGTON.
PI	Salkoff L, Schreiber M, Silvia C;
XX	
DR	WPI: 1999-326593/27.
XX	
PT	P-FSDB; AAK13442.
XX	
XX	Voltage-gated, pH-sensitive potassium channel useful in gene therapy

OY 1741 cgtaaagaacacattagggtttcttatctgtcgaactccaagaagacgtcgttg 1800
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DB 1741 cgtaaagaacacattagggtttcttatctgtcgaactccaagaagacgtcgttg 1800
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OY 1801 ttctactgttcagctcgtcagatgatgtgtctcatcttccttgagctaatatcaaacgttggc 1860
|||||
DB 1801 ttctactgttcagctcgtcagatgatgtgtctcatcttccttgagctaatatcaaacgttggc 1860
|||||
OY 1861 tgcataaagcagaagccggtcagacacatcagctgcgtatcgtataaagaatgataaanaagtc 1920
|||||
DB 1861 tgcataaagcagaagccggtcagacacatcagctgcgtatcgtataaagaatgataaanaagtc 1920
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OY 1921 ctggaaggaatctctctcgtatatacagggaggtcttcgcgcaaggggtatctcgaagc 1980
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DB 1921 ctggaaggaatctctctcgtatatacagggaggtcttcgcgcaaggggtatctcgaagc 1980
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OY 1981 acttcgagacatacaaaccttcaaccagagctcttcaacatgatatgtaaacagatctct 2040
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DB 1981 acttcgagacatacaaaccttcaaccagagctcttcaacatgatatgtaaacagatctct 2040
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DB 2041 gaccagcttgatagcagtggtgatgtttcactggtgcaaacacactcttggacaaggtg 2100
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OY 2161 ttctgagaatgcac 2220
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DB 2401 tcccccccaaccccgccatcaagaacacagacttggtagaagaagaagccatcatgtga 2460
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DB 3061 ccagccaatgtgattcaagctgctgcctcagatctgtgtttgtgcataccctcagc 3120
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DB 3121 actgtctgtataaagaagaatgaaagtctcattgcaaaagtcatatgaatgttaac 3180
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DB 3241 cagttactgagaacatgttatccacagctatcttaccagcggagaactaactccctc 3300
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DB 3301 ctttctcctaagaataag 3319
|||||
RESULT 2
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ID AAK55525 standard; DNA: 3247 BP.
XX
XX AAK55525;
AC
XX
DT 26-JUL-1999 (first entry)
XX
DE Nucleotide sequence of hSio3-2.
XX
XX
KW Voltage-gated; pH sensitive; potassium channel; Sio3; spermatocyte;
KW sperm capacitation; acrosome reaction; fertilization; infertility;
KW contraceptive; sperm physiology; channel protein; gene therapy; ss.
OS Homo sapiens.
XX
XX W09920754-A1.
PN
XX
PD 29-APR-1999.
XX
PF 21-OCT-1998; 98WO-US22321.
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XX
PR 27-FEB-1998; 98US-0076172.
PR 22-OCT-1997; 97US-0063138.
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XX (UNIW) UNIV WASHINGTON.
PA
XX
PI Salkoff L, Schreiber M, Silvia C;
XX
XX WPI: 1999-326593/27.
DR
XX P-PSDB; AAY13443.
XX
XX Voltage-gated, pH-sensitive potassium channel useful in gene therapy
PT
XX
PS Claim 9; Page 81-82; 93pp; English.
XX

CC The invention relates to a voltage-gated, pH sensitive potassium channel
CC S103, expressed in spermatoocytes. S103 has, as a monomer, calculated
CC molecular weight 120-156 kD; has unit conductance (as a functional
CC tetramer, when expressed in Xenopus oocytes) of 80-120 pS; has increased
CC activity at intracellular pH above about 7.1 and binds specifically to
CC polyclonal antibodies against sequences shown in AY13437, AY13438,
CC AY13442, and AY13443. S103 is involved in sperm capacitation and/or the
CC acrosome reaction, essential steps in fertilization. S103, and the
CC nucleic acid encoding it, are used to identify specific inhibitors and
CC activators (potentially useful for treating infertility and as
CC contraceptives), also for studying sperm physiology in vitro.
CC S103-specific antibodies are used for diagnostic detection of S103
CC expression. S103, as part of a chimera with another channel protein, can
CC be used as a reporter for measuring changes in potassium concentration,
CC current flow, ion flux, etc. Fragments of S103 nucleic acid are useful as
CC probes for identifying homologs, variants and mutants associated with
CC disease; to detect S103-related mRNA or protein; for chromosomal
CC localization; in gene therapy; for identifying potential modulators; to
CC measure up-regulation of S103 in drug screening assays and for production
CC of recombinant S103 protein. The present sequence represents the
CC nucleotide sequence of hS103-2.
CC
CC
XX

SO Sequence 3247 BP; 913 A; 740 C; 681 G; 912 T; 1 other;

Query Match 95.3% Score 3163.6; DB 20; Length 3247;
Best Local Similarity 97.8%; Pred. No. 0;
Matches 3246; Conservative 0; Mismatches 0; Indels 72; Gaps 1;

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DB 1 atgtttcagactaagctagcaagaacttggaagacttgcaaaaagtctgtgaca 60
OY 61 acgagagaccagaagcagatcatctctctctctctgtgacacctctcagtgagcatc 120
DB 61 acgagagaccagaagcagatcatctctctctctctgtgacacctctcagtgagcatc 120
OY 121 atccctgtgactctcagctgcatctgagagatcgttaaaaatggaacatcatcaaggga 180
DB 121 atccctgtgactctcagctgcatctgagagatcgttaaaaatggaacatcatcaaggga 180
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DB 361 ttcatcaatctcgtgacacctgtgtgagagctgttcatcatatgaagaacaaacatctcct 420
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OY 481 gatgagacaagtcaagtctgctgctgagagatgaatccaatcgtatagaacatcttaaccca 540
DB 481 gatgagacaagtcaagtctgctgctgagagatgaatccaatcgtatagaacatcttaaccca 540
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DB 541 ccaaaccttattcttattttgaagagacaattggtcttaagtgcttaagagcc 600
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DB 601 ttgagcctgtagaaactccatcaaatcttgcaaatcttaagagccatcaagacagtaac 660

OY 661 tcaatgaagtttccaaactcgtgtcatataattcgaatccctggtccacagctgtgga 720
DB 661 tcaatgaagtttccaaactcgtgtcatataattcgaatccctggtccacagctgtgga 720
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DB 721 ttcatcaatctcgtgagaaattctgtgtgacccgtgtcgaaggtagaattcaacaat 780
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DB 781 atatacatcttgatcaaatcttaacctgtcatgtgcaacaacgyltaacgttgatgga 840
OY 841 gatgtgttagccaagacatcccttagagagacacctcatatgtcttcacactgaggagt 900
DB 841 gatgtgttagccaagacatcccttagagagacacctcatatgtcttcacactgaggagt 900
OY 901 ttgatattatttggaactataaccctgaagaatggtgaactgtttgttaacaagaaggaa 960
DB 901 ttgatattatttggaactataaccctgaagaatggtgaactgtttgttaacaagaaggaa 960
OY 961 tacacagctctmtatgaagcactcaagaagaagtattatctgtgctgttgaaacatc 1020
DB 961 tacacagctctmtatgaagcactcaagaagaagtattatctgtgctgttgaaacatc 1020
OY 1021 actgttgacaagtgtgacgccttccctgaagaaattccctcgcgacaagtcagaagagatc 1080
DB 1021 actgttgacaagtgtgacgccttccctgaagaaattccctcgcgacaagtcagaagagatc 1080
OY 1081 aacacgtaaattcttcccgaggagaacccctcctctcttggaacttgaaacatatt 1140
DB 1081 aacacgtaaattcttcccgaggagaacccctcctctcttggaacttgaaacatatt 1140
OY 1141 aaatgctactcttgacctacacacagctcatctctgaaatctgaaatgaaatggaatctg 1200
DB 1141 aaatgctactcttgacctacacacagctcatctctgaaatctgaaatgaaatggaatctg 1200
OY 1201 aggcagagctgcgtgtgaaatctgcagaggaatgcctgataatagcaaatccctgtgcagt 1260
DB 1201 aggcagagctgcgtgtgaaatctgcagaggaatgcctgataatagcaaatccctgtgcagt 1260
OY 1261 gattcccatgctgaagaatatttccaacatattagaggtgtctctatacagaagactatgat 1320
DB 1261 gattcccatgctgaagaatatttccaacatattagaggtgtctctatacagaagactatgat 1320
OY 1321 tctacacacagaaatcatalcatagatactgaaatcccaatacaagaagtcttaactgtgccaag 1380
DB 1321 tctacacacagaaatcatalcatagatactgaaatcccaatacaagaagtcttaactgtgccaag 1380
OY 1381 attcccaagctggaactgtgagacacccggagacaacatactctgtctgtgataataaact 1440
DB 1381 attcccaagctggaactgtgagacacccggagacaacatactctgtctgtgataataaact 1440
OY 1441 ggaatttaccgccaagagcttctgtgtccagagctgtgtgacacctctcaacatctctat 1500
DB 1441 ggaatttaccgccaagagcttctgtgtccagagctgtgtgacacctctcaacatctctat 1500
OY 1501 gtgagagcaaaacaaaagttaatgacctaaacagacctggaagaacactctctgaatagc 1560
DB 1501 gtgagagcaaaacaaaagttaatgacctaaacagacctggaagaacactctctgaatagc 1560
OY 1561 atgaaaaaacaatttctgacccaagagctctctgatagaacttctgtgaaagaaactcttcc 1620
DB 1561 atgaaaaaacaatttctgacccaagagctctctgatagaacttctgtgaaagaaactcttcc 1620
OY 1621 gaagtgtccggtctctctctctgaagaatgtacactctgtgtgaagcactgaataaag 1680
DB 1621 gaagtgtccggtctctctctctgaagaatgtacactctgtgtgaagcactgaataaag 1680
OY 1681 tccctcttaacgagatgttctgtgtgtgatactaaatccacactccacaagtgaagata 1740
DB 1681 tccctcttaacgagatgttctgtgtgtgatactaaatccacactccacaagtgaagata 1740
OY 1741 cgtagaagacatattaggtctcttattctgtcgtgaatactccaagaagagcttcagaagagccttg 1800

```

Db 1669 cgtaagaacacatlagggttcttatttgctgaaactccaagaagctcgaagagccttg 1728
Oy 1801 ttttctcttcaagctctgtcaatgaatgtgttcaatctcttgagctaatcaaacctgtgc 1860
Db 1729 tttctcttctcagctctgtcatatgaatgtgttcaatctcgaagctaatcaaacctgtgc 1788
Oy 1861 tgcanaagcagaagccggaagcagacataccagctcagctgaagaagaaatgaanaatgt 1920
Db 1789 tgcanaagcagaagccggaagcagacataccagctcagctgaagaagaaatgaanaatgt 1848
Oy 1921 ctgaagggaatctctctctgtatatacagggcaggaattctcgcgcgaagggtatctgcaagc 1980
Db 1849 ctgaagggaatctctctctgtatatacagggcaggaattctcgcgcgaagggtatctgcaagc 1908
Oy 1981 actctgagacataatcaaatctcaccacaggaactctcaacatgaatgtagaacaagaattct 2040
Db 1909 actctgagacataatcaaatctcaccacaggaactctcaacatgaatgtagaacaagaattct 1968
Oy 2041 gaccagcttgatagcagtgagatgttctacgtgtgcaaaccaactctttggaacaagctg 2100
Db 1969 gaccagcttgatagcagtgagatgttctacgtgtgcaaaccaactctttggaacaagctg 2028
Oy 2101 actctgaaacgaactctgcaagtcgaagtcgaagtcgaagtcgaagtcgaagtcgaagtcga 2160
Db 2029 actctgaaacgaactctgcaagtcgaagtcgaagtcgaagtcgaagtcgaagtcgaagtcga 2088
Oy 2161 ttgtgagatgccaatctcagcccgatgggctctggaactctgttaatgtcccttgagaagcc 2220
Db 2089 ttgtgagatgccaatctcagcccgatgggctctggaactctgttaatgtcccttgagaagcc 2148
Oy 2221 agcaactatacagaagaagtcgaagtcgaagtcgaagtcgaagtcgaagtcgaagtcgaagtcga 2280
Db 2149 agcaactatacagaagaagtcgaagtcgaagtcgaagtcgaagtcgaagtcgaagtcgaagtcga 2208
Oy 2281 cagagaagaatgagcgaattctccggaattctcccgagataatacattctgcctgagatgtgca 2340
Db 2209 cagagaagaatgagcgaattctccggaattctcccgagataatacattctgcctgagatgtgca 2268
Oy 2341 ctttatcttgagagactctcattgctgcgcgaacataagagcaatgtctcatgtgtctgtcttg 2400
Db 2269 ctttatcttgagagactctcattgctgcgcgaacataagagcaatgtctcatgtgtctgtcttg 2328
Oy 2401 tcccccccaaccccaacatacgaagcaacaggaactctgtgtagacaagaacccatactgtgca 2460
Db 2329 tcccccccaaccccaacatacgaagcaacaggaactctgtgtagacaagaacccatactgtgca 2388
Oy 2461 accctcaacatctggaatccttgcgaatgtgactctcctctgaccgctcacctcagtgta 2520
Db 2389 accctcaacatctggaatccttgcgaatgtgactctcctctgaccgctcacctcagtgta 2448
Oy 2521 gaggagactcccggttaacaaatgagacataatgaagaatacaactgcccgaanaagctccct 2580
Db 2449 gaggagactcccggttaacaaatgagacataatgaagaatacaactgcccgaanaagctccct 2508
Oy 2581 atccctactgaactgaanaaatccctcccaacataccttattgaaacagcttggtgagactg 2640
Db 2509 atccctactgaactgaanaaatccctcccaacataccttattgaaacagcttggtgagactg 2568
Oy 2641 gaagggtccctcccaagaanaaatactgcatactcagcaactgtccttctctacgggcaactgtt 2700
Db 2569 gaagggtccctcccaagaanaaatactgcatactcagcaactgtccttctctacgggcaactgtt 2628
Oy 2701 ttttccagaagcttcttgatctctgtctgcccgaagccttctaanaattatattgtctcg 2760
Db 2629 ttttccagaagcttcttgatctctgtctgcccgaagccttctaanaattatattgtctcg 2688
Oy 2761 gaattgtctcagatgtctgtgacagagagtaagttctcagctggaacaacattagat 2820
Db 2689 gaattgtctcagatgtctgtgacagagagtaagttctcagctggaacaacattagat 2748
Oy 2821 aagataaagctatagtgtgtgacagatagctgcacgtctgtctgtctggaagaacgg 2880

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Db 2749 aagataaagctatagtgtgtgacagatagctgcacgtctctgtctgtctggaagaacgg 2808
Oy 2881 tgaagctggggctctctgtccttaacagaacacatttatacgaagcttaataccaagaaac 2940
Db 2809 tgaagctggggctctctgtccttaacagaacacatttatacgaagcttaataccaagaaac 2868
Oy 2941 acccttgacaactgtctgtgtccatagaaccttttggatccctgtgtgtgtgtgcta 3000
Db 2869 acccttgacaactgtctgtgtccatagaaccttttggatccctgtgtgtgtgtgcta 2928
Oy 3001 taccgaataatgtatgaagaagagctcaaacccagaanaaagggttltgtatcacccgg 3060
Db 2929 taccgaataatgtatgaagaagagctcaaacccagaanaaagggttltgtatcacccgg 2988
Oy 3061 ccagccaatgaatccaagctgtccttcaagatctgtgttltgtgccaataccttcagc 3120
Db 2989 ccagccaatgaatccaagctgtccttcaagatctgtgttltgtgccaataccttcagc 3048
Oy 3121 actgctgttataaagaagatgaagaagctctcatltgcaaaagtcataatgaatgttaaat 3180
Db 3049 actgctgttataaagaagatgaagaagctctcatltgcaaaagtcataatgaatgttaaat 3108
Oy 3181 aaagatcacagacaacagaagagacacatlcagacaacaaatgtlccctccacccatgtat 3240
Db 3109 aaagatcacagacaacagaagagacacatlcagacaacaaatgtlccctccacccatgtat 3168
Oy 3241 cagttactgagacatgttatccacagctctattcttaccagccggaataatccctct 3300
Db 3169 cagttactgagacatgttatccacagctctattcttaccagccggaataatccctct 3228
Oy 3301 ctttccctaagaacatag 3318
Db 3229 ctttccctaagaacatag 3246

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RESULT 3
AAK5514
ID AAK5514 standard; DNA; 3339 BP.
XX
AC AAK5514;
XX
DT 26-JUL-1999 (first entry)
XX
DE Mouse SLO3 (mSLO3) encoding DNA.
XX
KW Voltage-gated; pH sensitive; potassium channel; SLO3; spermatocyte;
KW sperm capacitation; acrosome reaction; fertilization; infertility;
KW contraceptive; sperm physiology; channel protein; gene therapy; ss.
XX
OS Mus sp.
XX
PN WO9920754-A1.
XX
PD 29-APR-1999.
XX
PE 21-OCT-1998; 98WO-US22321.
XX
PR 27-FEB-1998; 98US-0076172.
PR 22-OCT-1997; 97US-0063138.
XX
PA (UNITM ) UNITV WASHINGTON.
PI Salkoff L, Schreiber M, Silva C;
DR WPT: 1999-326593/27.
XX
PS P-PSDB: AAV13437.
XX
PS Voltage-gated, pH-sensitive potassium channel useful in gene therapy
XX
PS Claim 8; Page 77-78; 93pp; English.
XX
CC The invention relates to a voltage-gated, pH sensitive potassium channel
CC SLO3, expressed in spermatoocytes. SLO3 has, as a monomer, calculated

```


1801 ttctactgtcagctcgtcactgatgtgtcattccctcgtgacataacaaactgtgc 1860
1798 ttctacgtctccaaactgtccacagagatgtgtgcattccctgtgacataatgtgtaac 1857
1861 tgcgaagcagaagcgcgcgcacacatcagtgccatcgtctaaagagaatgaanaatgtc 1920
1858 tgcataacaaagccgcgaacaaactcaagacccacatcatgtgtatgaagacagc 1917
1921 ctgaaggaactctctcgtatatacagagatcttcgcgaaggtatct----- 1974
1918 tgcacggaattccaaactctctccacacatccacgctctatgtccacgaatcacact 1977
1975 -----gcgaagcattcgacatccacacatccacacacgaagcccttcacact 2022
1978 tgttttcaagaagacagccatgttgcattacatcaacacacagccacagcaaac 2037
2023 gatctagaacaagaattctgcacagcttgatagcagtgagatgttctactgtgcacaaca 2082
2038 gacacagtggaatgataccgacatgtgcagacagtgagcatgttctactgtgcagagca 2097
2083 accctctggacgaagtgtaacctgaagaactgcgaatcgaatataagtttcggaac 2142
2098 atgcctctggacgaagtggtctcgaagagtgagaggaagaacacgagatltcagaac 2157
2143 catactgtagcatgtgtaattcggagatgccacacagcccgatgggcttcggaactt 2202
2158 caeatgtgtagtgcgtgtgttgagagatgcccaatgtaccctggtgtggtcttcggaattc 2217
2203 gtaatgcccttgagagcagacgaacatacgaagaagagctgaagagacatagtgtcat 2262
2218 gtgattgccccgagagcagacgaacacacccgcgcagagctgaagagacatgttttatt 2277
2263 gggctctcgagctatctcaagaagaatgagcttctccggaatttccccagataac 2322
2278 gggctctcgagctatctcaagaagaatgagcttctccggaatttccccagataac 2337
2323 attctgcctgtagtgcacattatcttcgagacatccatccatcgccgaacatagagaatgc 2382
2338 attatgctgtgtagtgcacatctacatgagatcgtatgtcagatcaatgtagagagatgc 2397
2383 tccatgtgtgtgtctgttcccccacccacagacatcaagaacagacttctgttagac 2442
2398 tctatgtgtgtgtctgttcccccacccacagacatcaagaacagacttctgttagac 2457
2443 acgaagaagcattcagacacccctacatccatcgtatctgtcaaatgtactctctctgac 2502
2458 acgaagaagcattcagacacccctacatccatcgtatctgtcaaatgtactctctctgac 2517
2503 ccgtcacacctcagtgtagagagagatccaggttacacaaatgagacataatgagaatca 2562
2518 gggctctcaagaatcagaagtaagacacatcctgctttagatgaagaagaagaagaa 2577
2563 aactgcgaagaagctccatctctactcgtactgaactgaanaaactcttccaaacttatt 2622
2578 agatacaaaacagatctccatctctcactgaactgaagaatctccctccaaactattatt 2637
2633 gaacagctgtgtgtagcgtgaagaggtccctccaaagaacaaatctgcattcagacatgcc 2682
2638 gageagagtgagcgtgtagcgtgaagaggtccctccaaagaacaaatctgcattcagacatgcc 2697
2683 tttctacagcagcagcttctccagcagctctgtgactcgtctcgtccagcagcttc 2742
2698 tttccacacggtgtgtcttctccagcagctctgtgactcgtctcgtccagcagcttc 2757
2743 tacaattatcagctcgtgaatgtctcagatgtcgtgtagcagagagagtaagtctcag 2802
2758 tacaattatcagctcgtgaatgtctcagatgtcgtgtagcagagagagtaagtctcag 2817
2803 ctggaacaacatttagaataagataagctcagatgtgtgtagcagatagctgcagctgc 2862
2818 atggaacacatttgttaagaagaagacccataaagacacacagcagcattatgaaggacac 2877

2863 ttgtctgaagaagaacggtgaagcgtgggctctgtctcttaccagaacacattatca 2922
2878 aagctgtggaagagcgggtgtaagctgtgagctccctcttaccagaacacattatca 2937
2923 gacgttaatccaagaagaacacacttggacacatgtctgtgctcattatgactcttgg 2982
2938 ggcattatccaagaagaacacacttggacacatgtctgtgctcattatgactcttgg 2997
2983 atccgtgtgtgtgtgttaccgaataatgtatgaagagagagctcaacccaagaacaa 3042
2998 atccatgtgtgtgtgtgttaccgaataatgtatgaagagagagctcaacccaagaacaa 3057
3043 aggttctgtagcaccgagcagacatgattcgaagctgcgtcctcagatctgtctt 3102
3058 aggttctgtagcaccgagcagacatgattcgaagctgcgtcctcagatctgtctt 3117
3103 ttgtccataccctcagcagctgtgttataaa 3135
3118 ttgtccataccctcagcagctgtgttataaa 3150

RESULT 4

AAK5515 standard; DNA: 416 BP.

AAK5515;

26-JUL-1999 (first entry)

Human SLO3 (hSLO3) encoding DNA.

Voltage-gated: pH sensitive; potassium channel; SLO3; spermatocyte; sperm capacitation; acrosome reaction; fertilization; infertility; contraceptive; sperm physiology; channel protein; gene therapy; ss.

Homo sapiens.

MO9920754-A1.

29-APR-1999.

21-OCT-1998; 98WO-US22321.

27-FEB-1998; 98US-0076172.

22-OCT-1997; 97US-0063138.

(UNIM) UNIV WASHINGTON.

SalKoff L, Schreiber M, Silvia C;

WPI: 1999-326593/27.

P-PSDB: AAY13438.

Voltage-gated, pH-sensitive potassium channel useful in gene therapy

Claim 9; Page 78-79; 93pp; English.

The invention relates to a voltage-gated, pH sensitive potassium channel SLO3, expressed in spermatoocytes. SLO3 has, as a monomer, calculated molecular weight 120-156 kD; has unit conductance (as a functional tetramer, when expressed in *Xenopus* oocytes) of 80-120 pS; has increased activity at intracellular pH above about 7.1 and binds specifically to polyclonal antibodies against sequences shown in AAY13437, AAY13438, AAY13442, and AAY13443. SLO3 is involved in sperm capacitation and/or the acrosome reaction, essential steps in fertilization. SLO3, and the nucleic acid encoding it, are used to identify specific inhibitors and activators (potentially useful for treating infertility and as contraceptives), also for studying sperm physiology in vitro. SLO3-specific antibodies are used for diagnostic detection of SLO3 expression. SLO3, as part of a chimera with another channel protein, can be used as a reporter for measuring changes in potassium concentration, current flow, ion flux, etc. Fragments of SLO3 nucleic acid are useful as probes for identifying homologs, variants and mutants associated with

AAFS8254/C
ID AAF58254 standard; DNA: 936 BP.
XX
AC AAF58254;
XX
XX
XX 24-APR-2001 (first entry)
XX
XX Oligonucleotide D1875.
XX
XX
XX Electron-transfer group; ETM; mismatch; genotyping;
KW gene expression; ss.
XX
XX Synthetic.
XX
XX WO200107665-A2.
XX
XX 01-FEB-2001.
XX
XX 26-JUL-2000; 2000WO-US20476.
XX
XX 26-JUL-1999; 99US-0145695.
XX 17-MAR-2000; 2000US-0190259.
XX
XX (CLIN-) CLINICAL MICRO SENSORS INC.
XX
XX Umek RM;
XX
XX WPI: 2001-159728/16.
XX
XX Nucleic acids containing electron-transfer group, useful as labels in
PT hybridization assays, e.g. for genotyping, allowing repeat analyses on
PT a single surface
XX
XX Example 6; Page 127; 159pp; English.
XX
XX The present invention relates to a composition comprising two nucleic
CC acids each containing an electron-transfer group (ETM) having
CC different redox potentials. The invention is used for electronic
CC detection of nucleic acids, especially of substitutions (mismatches)
CC and single-nucleotide polymorphisms, e.g. for genotyping,
CC monitoring gene expression.
XX
XX
SQ Sequence 936 BP; 4 A; 144 C; 7 G; 5 T; 776 other;

Query Match 2.8%; Score 94.4; DB 22; Length 936;
Best Local Similarity 0.7%; Pred. No. 4,3e-17;
Matches 5; Conservative 445; Mismatches 296; Indels 0; Gaps 0;

OY 257 aattcgatcatatagaaatggtgcttcagccagacctgtggggcaagtctgg 316
DB 754 ww 695
OY 317 tgatcctgctcttgtaagaacatgggtctctataatcattcaatctgctg 376
DB 694 ww 635
OY 377 acccgctgggaagcgtcatcatatgaagacaacacatctctattgtttcca 436
DB 634 ww 575
OY 437 atgcttcttgatcttcatttgatgaggttcatgcaagctgacgaagatcaagt 496
DB 574 ww 515
OY 497 tctgctcgagatgaatcacaatcagacatcttaccatccacaacatttctt 556
DB 514 ww 455
OY 557 attattgaaagcaatgctgaggttcaaggttctctaagagccttgccctgtagaac 616
DB 454 ww 395

OY 617 tccctcaaatcttgcaaatctcagacatcaagaaccagtaactgtaagtttcca 676
DB 394 AGCww 335
OY 677 aactgctgcataatctctcagttcagttcacaagcgcgggattcaatccctggtg 736
DB 334 ww 275
OY 737 aaattctggtgattccctcgctcaaggttagaatctcagatatatttgagt 796
DB 274 ww 215
OY 797 caattacactggtlcatggaacaacgtaaccggttggatttgagatgtgtagcaaga 856
DB 214 ww 155
OY 857 catccttagagcagacctcatcatgtctctcacaacgtgggagttgatatattgca 916
DB 154 ww 95
OY 917 actatataccctgaatgtgtggaactgttgcctacaagaaggaatacacccagttcmtatg 976
DB 94 ww 35
OY 977 aagcactcaaggaagaagtattt 1002
DB 34 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 9

RESULT 7
AAFS8257/C
ID AAF58257 standard; DNA: 936 BP.
XX
XX AAF58257;
XX
XX 24-APR-2001 (first entry)
XX
XX Oligonucleotide D1954.
XX
XX Electron-transfer group; ETM; mismatch; genotyping;
KW gene expression; ss.
XX
XX
XX Synthetic.
XX
XX WO200107665-A2.
XX
XX 01-FEB-2001.
XX
XX 26-JUL-2000; 2000WO-US20476.
XX
XX 26-JUL-1999; 99US-0145695.
XX 17-MAR-2000; 2000US-0190259.
XX
XX (CLIN-) CLINICAL MICRO SENSORS INC.
XX
XX Umek RM;
XX
XX WPI: 2001-159728/16.
XX
XX Nucleic acids containing electron-transfer group, useful as labels in
PT hybridization assays, e.g. for genotyping, allowing repeat analyses on
PT a single surface
XX
XX Example 6; Page 127; 159pp; English.
XX
XX The present invention relates to a composition comprising two nucleic
CC acids each containing an electron-transfer group (ETM) having
CC different redox potentials. The invention is used for electronic
CC detection of nucleic acids, especially of substitutions (mismatches)
CC and single-nucleotide polymorphisms, e.g. for genotyping,
CC monitoring gene expression.
XX
XX
SQ Sequence 936 BP; 5 A; 142 C; 7 G; 6 T; 776 other;


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Db 214 WWWWWW... 155
Qy 857 catccttagagcagcctcatalgtctcacaacgaggagttgatattgcga 916
Db 154 WWWWWW... 95
Qy 917 actatacctgaaatgtgtgaactgttgcatacaagaggaatacccgctcmctg 976
Db 94 WWWWWW... 35
Qy 977 aagcactcaagaagaagtattc 1002
Db 34 WWWWWW... 9

RESULT 9
AAFS8262/c
ID AAF58262 standard; DNA; 936 BP.
XX
AC AAF58262;
XX
DT 24-APR-2001 (first entry)
XX
DE Oligonucleotide D2007.
XX
KW Electron-transfer group; ETM; mismatch; genotyping;
   gene expression; ss.
XX
OS Synthetic.
XX
PN WO200107665-A2.
XX
PD 01-FEB-2001.
XX
PE 26-JUL-2000; 2000WO-US20476.
XX
PR 26-JUL-1999; 99US-0145695.
PR 17-MAR-2000; 2000US-0190259.
XX
PA (CLIN-) CLINICAL MICRO SENSORS INC.
XX
PI Umek RM;
XX
DR WPI; 2001-159728/16.
XX
PT Nucleic acids containing electron-transfer group, useful as labels in
   hybridization assays, e.g. for genotyping, allowing repeat analyses on
   a single surface.
XX
PS Example 6; Page 128; 159pp; English.
XX
CC The present invention relates to a composition comprising two nucleic
   acids each containing an electron-transfer group (ETM) having
   different redox potentials. The invention is used for electronic
   detection of nucleic acids, especially of substitutions (mismatches)
   and single-nucleotide polymorphisms, e.g. for genotyping,
   monitoring gene expression.
XX
SQ Sequence 936 BP; 5 A; 139 C; 10 G; 6 T; 776 other;

Query Match      2.8%; Score 94.4; DB 22; Length 936;
Best Local Similarity 0.7%; Pred. No. 4,3e-17;
Matches 5; Conservative 445; Mismatches 296; Indels 0; Gaps 0;
```

```
Qy 377 accctgtggaagcgtgtcatalcatatgaaagaaaccatcctattgattgttcca 436
Db 634 WWWWWW... 575
Qy 437 atgcttcttagtttcatcttcttgatgagttttagcgcgatgacaagatcaagt 496
Db 574 WWWWWW... 515
Qy 497 tctgctgagatgaatcaatcgttagacatcttaccatcccaaccttattct 556
Db 514 WWWWWW... 455
Qy 557 attattgaaagacatgtgctgaagtttaagttccctcaagcctgtgcctgctagaac 616
Db 454 WWWWWW... 395
Qy 617 tccctcaatctgcaatcttacaagcacaagcagtaactcagtgaaatttcca 676
Db 394 AGCWWWWW... 335
Qy 677 aactgctgcaataatctcagtaacctgtgtacaagctgcggattcacaacctgtg 736
Db 334 WWWWWW... 275
Qy 737 aaattctgtgatccctgcgtcacaaggtagaatctcacaatatatcatatttggt 796
Db 274 WWWWWW... 215
Qy 797 caatttacctgtcatgcaacaacgltcaacctgttgatgtgagatgtgtagccaaga 856
Db 214 WWWWWW... 155
Qy 857 catccttagagcagcctcatalgtctcacaacgaggagttgatattgcga 916
Db 154 WWWWWW... 95
Qy 917 actatacctgaaatgtgtgaactgttgcatacaagaggaatacccgctcmctg 976
Db 94 WWWWWW... 35
Qy 977 aagcactcaagaagaagtattc 1002
Db 34 WWWWWW... 9

RESULT 10
AAFS8255/c
ID AAF58255 standard; DNA; 938 BP.
XX
AC AAF58255;
XX
DT 24-APR-2001 (first entry)
XX
DE Oligonucleotide D1876.
XX
KW Electron-transfer group; ETM; mismatch; genotyping;
   gene expression; ss.
XX
OS Synthetic.
XX
PN WO200107665-A2.
XX
PD 01-FEB-2001.
XX
PE 26-JUL-2000; 2000WO-US20476.
XX
PR 26-JUL-1999; 99US-0145695.
PR 17-MAR-2000; 2000US-0190259.
XX
PA (CLIN-) CLINICAL MICRO SENSORS INC.
XX
PI Umek RM;
```



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Oy 623 aaatctgcaaatctacagacatcaagacagtaactcagtgagtttccaaactgc 682
::: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 303 www. .... 362
Oy 683 tgcataataatctcagtaactcgtgtcacagctgcggatcaatcactggtggaat 742
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 363 www. .... 422
Oy 743 ctgtgatccctgctcaagtagaattcacagaaatataatatttgatcaattc 802
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 423 www. .... 482
Oy 803 acctggtatgcacaacagtcacacgttgattgtgagatggtgagccaagacatcct 862
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 483 www. .... 542
Oy 863 tagagcagactcactcatgtctcacaactgaggagttgatatatttgcgaactata 922
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 543 www. .... 602
Oy 923 taactgaaatggtggaactgtttgtctaaagaagaaatacacacagttcmtatgaagcac 982
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 603 www. .... 662
Oy 983 tcaagaagaagaagtttatgtgtctgtggaacatcacgttgacagtgtagaccgtt 1042
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 663 www. .... 722
Oy 1043 tctctgagaatttctcctcgacagaagtcagagatcaacactgaaatctgttctctgg 1102
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 723 www. .... 782
Oy 1103 gagaacccctcc 1115
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 783 wwwgcccccc 795

RESULT 12
AAF58254
ID AAF58254 standard; DNA; 936 BP.
XX
AC AAF58254;
XX
DT 24-APR-2001 (first entry)
XX
DE Oligonucleotide D1875.
XX
KW Electron-transfer group; ETM; mismatch; genotyping;
KM gene expression; ss.
XX
OS Synthetic.
XX
PN W0200107665-A2.
XX
PD 01-FEB-2001.
XX
PE 26-JUL-2000; 2000MO-US20476.
XX
PR 26-JUL-1999; 99US-0145695.
PR 17-MAR-2000; 2000US-0190259.
XX
PA (CLIN-) CLINICAL MICRO SENSORS INC.
XX
PI Umek RM;
XX
DR WPI; 2001-159728/16.
XX
PT Nucleic acids containing electron-transfer group, useful as labels in
PT hybridization assays, e.g. for genotyping, allowing repeat analyses on
XX a single surface
XX
PS Example 6; Page 127; 159p; English.
```

```
CC The present invention relates to a composition comprising two nucleic
CC acids each containing an electron-transfer group (ETM) having
CC different redox potentials. The invention is used for electronic
CC detection of nucleic acids, especially of substitutions (mismatches)
CC and single-nucleotide polymorphisms, e.g. for genotyping,
CC monitoring gene expression.
XX
SQ Sequence 936 BP; 4 A; 144 C; 7 G; 5 T; 776 other;
```

```
Query Match 2.88; Score 93.4; DB 22; Length 936;
Best Local Similarity 1.3%; Pred. No. 8.3e-17;
Matches 10; Conservative 461; Mismatches 322; Indels 0; Gaps 0;
```

```
Oy 323 ttgtcttctctaagcattggtctctataatctatcaatctctcgaacctg 382
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 3 www. .... 62
Oy 383 ttggaagctgtcatcatatgaagacaacacatccattgatttgtttcaatgctt 442
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 63 www. .... 122
Oy 443 tctttagttctatcttgataggttatagtgcagctgatacaagaatcaagttctggc 502
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 123 www. .... 182
Oy 503 tggagatgaattcaatcgttagacatcttaccatcccaaccttctctatctt 562
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 183 www. .... 242
Oy 563 tgaagaagaattggttaggtttaaagttcctaagaagcttcgctgttagaacctctc 622
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 243 www. .... 302
Oy 623 aaatctgcaaatctacagacatcaagacagtaactcagtgagtttccaaactgc 682
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 303 www. .... 362
Oy 683 tgcataataatctcagtcctcgtgtcacagctgcgggttcatcactggtggaatc 742
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 363 www. .... 422
Oy 743 ctgtgatccctggtcacaagtagaattcacagaatatataatatttgatcaattc 802
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 423 www. .... 482
Oy 803 acctggtcatgcacaacagtcacacgttgattgtgagatggtgtagccaagacatcct 862
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 483 www. .... 542
Oy 863 tagagcagactcactcatgttcttcaacactgaggagttgatatatttgcgaactata 922
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 543 www. .... 602
Oy 923 taactgaaatggtggaactgtttgtctaaagaagaaatacacacagttcmtatgaagcac 982
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 603 www. .... 662
Oy 983 tcaagaagaagaagtttatgtgtctgtggaacatcacactgtgacagtgtagaccgtt 1042
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 663 www. .... 722
Oy 1043 tctctgagaatttctcctcgacagaagtcagagatcaacactgaaatctgttctctgg 1102
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 723 www. .... 782
Oy 1103 gagaacccctcc 1115
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 783 wwwgcccccc 795

RESULT 13
AAF58257
```


CC monitoring gene expression.

XX Sequence 936 BP; 6 A; 138 C; 8 G; 8 T; 776 other;

Query Match 2.8%; Score 93.4; DB 22; Length 936;

Best Local Similarity 1.3%; Pred. No. 8.3e-17;
Matches 10; Conservative 461; Mismatches 322; Indels 0; Gaps 0;

```
OY 323 ttgcttctgaagcattggtctctataatctatcatcatctctgacctg 382
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 3 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 62

OY 383 ttggaagctgtcatcatatgaagaacaacattcctatgatttggttcaatgctt 442
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 63 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 122

OY 443 tcttagttctatttggattgagttatgagcagctgataagaatcaagtctgac 502
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 123 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 182

OY 503 tggagatgaattcaatcgttagacatttaccaccacacatttctctattt 562
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 183 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 242

OY 563 tgaagagcaattgcttagtttaagttcctagaagccttgccgtgtagaactccctc 622
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 243 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 302

OY 623 aaatcttgcaaatcttaagacatcaagaccgaactgaagtttccaaactgc 682
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 303 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 362

OY 683 tgtcaataatctcaagtcacctggttcaagctgcggagttcaatcactggtgtaaatc 742
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 363 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 422

OY 743 ctggtgacccctgctcaaggtagaattcacagaatatcatatttgaatcatt 802
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 423 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 482

OY 803 acctgtgcatgcaacaacgctcaacgcttgatttgagatggtgtagcaagacatcct 862
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 483 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 542

OY 863 tagaagcgaacttcaatcgttcttcaacacgaggagttgatatatttcgaaacta 922
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 543 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 602

OY 923 taactgaatggtggaactgtttgtctaaagaagaaatataccagttcmtatgagcac 982
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 603 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 662

OY 983 tcaagaagaagaatttatttggtctctggaacaatcaactgtgagactgtgacctt 1042
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 663 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 722

OY 1043 tctcgtggaatttctcctcgacaaagtcagagagatacaacactgaaatttcttctcgtg 1102
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 723 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 782

OY 1103 gagaacccctcc 1115
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 783 wwwwwwgccccccc 795
```

RESULT 15

AAFS8262

AC AAF58262;

DT 24-APR-2001 (first entry)

XX Oligonucleotide D2007.

XX Electron-transfer group; ETM; mismatch; genotyping;

XX gene expression; ss.

XX Synthetic.

XX WO200107665-A2.

XX 01-FEB-2001.

XX 26-JUL-2000; 2000WO-US20476.

XX 26-JUL-1999; 99US-0145695.

XX 17-MAR-2000; 2000US-0190259.

(CLIN-) CLINICAL MICRO SENSORS INC.

XX Umek RM;

XX WPI: 2001-159728/16.

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XX detection of nucleic acids, especially of substitutions (mismatches)
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SQ Sequence 936 BP; 5 A; 139 C; 10 G; 6 T; 776 other;

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Matches 10; Conservative 461; Mismatches 322; Indels 0; Gaps 0;

```
OY 323 ttgcttctgaagcattggtctctataatctatcatcatctctgacctg 382
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 3 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 62

OY 383 ttggaagctgtcatcatatgaagaacaacattcctatgatttggttcaatgctt 442
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 63 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 122

OY 443 tcttagttctatttggattgagttatgagcagctgataagaatcaagtctgac 502
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 123 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 182

OY 503 tggagatgaattcaatcgttagacatttaccaccacacatttctctattt 562
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 183 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 242

OY 563 tgaagaagaatggttagtttaagttcctaaagccttgccctgtagaactccctc 622
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 243 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 302

OY 623 aaatcttgcaaatcttaagacatcaagaccgaactgaagtttccaaactgc 682
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 303 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 362

OY 683 tgtcaataatctcaagtcacctggttcaagctgcggagttcaatcactggtgtaaatc 742
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 363 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 422

OY 743 ctggtgacccctgctcaaggtagaattcacagaatatcatatttgaatcatt 802
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 423 wwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwwww 482
```

Db	423	www.....	482
Qy	803	acctgfgtcafygcacaacgctcaacogltgagattgtagccaagacatcct	862
Db	483	www.....	542
Qy	863	taggaagacctcatcatgcttcttcaacactggaggttgattatattgtgaaacta	922
Db	543	www.....	602
Qy	923	tacctgaatfygtggaacttctgtctaacaagaggaaatacacagttomtaatgaacac	982
Db	603	www.....	662
Qy	983	tcaaaagaaagaagtattatgtgctctgfygaacaatacactgtgacagtytgaccgctt	1042
Db	663	www.....	722
Qy	1043	tccctgaggaatttctctccgcgacaagtctaggagatcaacactgaattgtttccctgg	1102
Db	723	www.....	782
Qy	1103	gagaaccctcc 115	
Db	783	wwwgccccccc 795	

Search completed: October 7, 2001, 19:19:14
Job time: 44493 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 7, 2001, 14:49:10 ; Search time 17859.3 Seconds

(without alignments)
2874.546 Million cell updates/sec

Title: US-09-176-664-17

Perfect score: 3319
Sequence: 1 atgttcagacaagctacg.....tctttcctaagaatagg 3319

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 7733874588 residues

Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

GenDbml:*

1: gb_ba1:*
2: gb_ba2:*
3: gb_ba3:*
4: gb_in1:*
5: gb_in2:*
6: gb_in3:*
7: gb_om:*
8: gb_ov:*
9: gb_pat1:*
10: gb_pat2:*
11: gb_ph:*
12: gb_pl1:*
13: gb_pl2:*
14: gb_pl3:*
15: gb_pl4:*
16: em_ba1:*
17: em_ba2:*
18: em_fun:*
19: em_htgo_hum:*
20: em_htgo_inv:*
21: em_htgo_rod:*
22: em_htg_hum1:*
23: em_htg_hum2:*
24: em_htg_hum3:*
25: em_htg_hum4:*
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27: em_htg_hum6:*
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30: em_htg_inv1:*
31: em_htg_inv2:*
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33: em_htg_rod:*
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35: em_hum2:*
36: em_hum3:*
37: em_hum4:*
38: em_hum5:*
39: em_hum6:*
40: em_hum7:*
41: em_in:*
42: em_om:*
43: em_or:*

44: em_ov:*
45: em_pat:*
46: em_ph:*
47: em_pl:*
48: em_ro:*
49: em_sts:*
50: em_sy:*
51: em_un:*
52: em_vi:*
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89: gb_pr5:*
90: gb_pr6:*
91: gb_pr7:*
92: gb_pr8:*
93: gb_pr9:*
94: gb_tol:*
95: gb_tol2:*
96: gb_in4:*
97: gb_pr10:*
98: em_ba3:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1857	56.0	3339	94 AF039213	AF039213 Mus muscu
2	705	21.2	3591	94 MUSMSLO	I16912 Mouse mslo
3	704.2	21.2	3456	88 AF026001	AF026001 Macaca mu
4	704	21.2	3459	7 AF026000	AF026000 Sus scrofa
5	697.8	21.0	3364	89 AF118141	AF118141 Homo sapi
6	697.8	21.0	3537	97 HS023767	U23767 Human calcl
7	697.8	21.0	5829	97 HS011058	U11058 Homo sapien
8	696.6	21.0	3581	8 AF036626	AF036626 Trechymys

Qy	541	ccacacccttattctctattattttgaaagcaatttgcctcaggtttcaagtttccctaagcc	600
Db	541	CCAACCTCTTAATTTCTTAATTAATTTGAAGAGTAATTTGGCTAAGTTTGAGATTCTTAAGAGCT	600
Qy	601	ctgcgcctctgctaaactccctccaactctctgcaactctctacgacccatcaagaacagctaac	660
Db	601	CTGGGGTGGTGCAGACTCCCTAAATCTTACGATTCCTTACAAAGTCATCAACACAGCAAT	660
Qy	661	tcagttgaagttctccaaactgcctgtccaataattctcagtaacctggtttccacagcttgcgga	720
Db	661	TCAGTGAAGCTTTCCAAACCTGTTGTCTCAAAATGTTATCACTACTGGTTTCACCGCAGCAGGA	720
Qy	721	ttcaatcaaccttggctggaataattctctgtatcccttgcccaagaagtgagaaatccagaat	780
Db	721	TTCCCTTACTCGGTGGGAAAATCTGGTGAACCCCTGGCTCAACGGAGAAGAACTCACACACT	780
Qy	781	atacatalattttgagttcaaatcttaacctgtgtacatgctgagcaaacagctcaacctgtttga	840
Db	781	ATGCATACTCTTGTAGCTCTATTATCTGTGGTGACAGACAAATGTCAACTGTTGCTGGTGGG	840
Qy	841	gagtggttagccaaagacatcccttaagacggaacctcatcagttcttcaaccttgaggagt	900
Db	841	GAGCTGGTGGCCAAAGACATCCCTTAGAGACGGATTCTTCATGTTTCTTCACCTTGGGAGT	900
Qy	901	ctgatactattctcgacaactataataaccttgaaatggtgtgaactgtttgtctaaacaaggaaa	960
Db	901	TTGATTAATAATTTGCCAAGCTACATCTCCAGAAATGGTGGAGCTCTTTCTACACAGGAAGAA	960
Qy	961	tcaaccagttcmtatgaaagcaatcaaaaggaagaattatgtgtctgtgtgaaacatc	1020
Db	961	TACACACAGGCTCTACAGACAGAGTCAAAAGGAAAAAGTTCACTGTGTGTGTGGAAACATC	1020
Qy	1021	acgtgtgaacaggttgagccgctcttcctcgtgaggaatttccctccgagaaagtcaagagagatc	1080
Db	1021	ACAGTTTACAGTGTACTGCTTTCCTCGAAGAAATTTTCTCCACTGGAATCCGGGGAAATC	1080
Qy	1081	aaacactgaaattgtttctcctgaggagaaccctcctctctcttggaaacttgaaacatatc	1140
Db	1081	AATTTTCAGATCTTAATTTCTTCTTGGAGAGACTCTCCCTTGCTTGGAACTGGAACCTTTACTG	1140
Qy	1141	aaatgctacacttgccctcaagaacaaagtctcatcttttgtatcgtgaatgaatgaggaagatcgt	1200
Db	1141	AAGTGCACACACATCTCTGTACCAACTTCTGTATGCGGCACCGCACTGAATTTGGAGGATCTG	1200
Qy	1201	agggcagttctgcggttggaatctcgtagagagatcgcctgatatataagccaactccttggagtt	1260
Db	1201	AAGGAGTTTGCAGTGGGAGAACTGGAGGGCTGCTGATTTCTAGCCAAACATTTCTGTAAT	1260
Qy	1261	gattcccaatgcgtgaagatatcttccaaactatagaagggtgtctctctatcaagaactatgatc	1320
Db	1261	GACTTACATATACCAAGACAACCTTAAACATTTATGAGGGTGTCTCGATTAACAACTATTAT	1320
Qy	1321	tctacccaccgaatactacatacagataactgcaatcccatcaacaaggtttactctgccaagt	1380
Db	1321	CCACAGACAGAGTCACTCATCTTCAATCTTCACTGATCTCAAAACAAAGTTTCTCTGTCAAAA	1380
Qy	1381	attcccaagcttggaacttggaacaccggaagaacaatcatcattgcttctgtcgtgaatlaaactt	1440
Db	1381	ATCCCCCAACTGGGAGCTGAGTCTGTGGAGACAATATCTCTGCTTGGCAGACTTAAAGCTC	1440
Qy	1441	ggattttctgcaccagaagctctgtgtggtgcagaagctgtgtactcttccataactctctatc	1500
Db	1441	GGATTTTATGCGCCCAAGGCTGTGTGGTGCCAGGGCTGTGACCTTTCTCTACGACTCTGTTC	1500
Qy	1501	gttgagagaaaaaaagaagttctatgctcttaaacagaccttggaagaaaacactcttgaatagc	1560
Db	1501	ATTTGAACAAAACCAAAAGGTTTTTCTTAACAATCCCTGGCAAAAACATTTCTTGATAGGC	1560
Qy	1561	atgaaaaaacaataattctgacccaagctctctctgtatgacttgcgtgtgaatgaagcttccct	1620
Db	1561	TTTGAAGAACAAGATTCTTGACACAGCCCTCTCTTAACGACTTGTGTGGGATGATCAATTTGCC	1620

QY	1621	gaagttgccggcgtctgtcttcttgaaagatgtaacccctcglttgatgcacatgaaataaag	1680
Db	1621	CAGGTCCTCCGGCTCTGGTTGTGTAAGGTAATAATTCATATGCTGATGCGCATCTCCAAACAG	1680
QY	1681	tccctcttaagaaTggtttctgtgtcgtgtaactaaatccaaacctcaagtgagaTta	1740
Db	1681	CCCTTCTTT---CACAGTTTGTGCACCTGTGATACTAAACCCTCATCTCCMACTGAGCTG	1737
QY	1741	cgtaagaacacatlaaggtttcttaattgtctgnaactccaaagaaagcgtlcagaagccttg	1800
Db	1738	AATAAGACACACTTGGGCTTCTTCAATGTGGAGCTCCTCCAAAGGCGGTCAAAAAGGCTTTC	1797
QY	1801	tttaactgttcagtcgtgtcgaTgaTgaTgTgttcaattctcttgagctaaattacaacTgTgc	1860
Db	1798	TTTTTACTGTTCMACTGTGCACGCGCATATGTGTCAATCTGTGACTTAATTGGAAAGTGTAC	1857
QY	1861	tgcaaagaacgaagccggcgaacacatcaacagTgcacatcgtaagaagatgaaanaTgt	1920
Db	1858	TCTAAAATCAAGAGCCGCAACAACTCATATGACCCGACCATCATGTGTATGTAAGAACAGC	1917
QY	1921	ctgaaggggaatctccctctcgtatatacaagggcaggaTctctcgccaaaggtatct-----	1974
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QY	2083	acctctctggaacaaTgtaactctgaaacgaacTggcgaagTcaaaTataagTtctggaac	2142
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QY	2263	gggtctctggaactatacaagaagaatgTgcgatttctctcggaattcttcccagaTatac	2322
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QY	2383	tccaatgtgtgcgtctgtgtgcccccccaaccccgagccataaagaacaaagacttggTgaagc	2442
Db	2398	TCTATGTGGTCATCTTAAGCCACACCCCTTACAAAGGCACTGAGCAGCCAGATTTCTGGTGGAC	2457
QY	2443	acagaagacatatTggaacccctccaaactcTgatactcttgaatTgaatcTccctctctgac	2502
Db	2458	ACAGAGGCCATATATGGCCACCTCAACATCCAGTCTCTGGGATCAGCAGTCTTACTTCCA	2517
QY	2503	ccgtcaacccTcagTgTcgaaggaagactccaggtTacaacaatTggaacataTgagaabaTca	2562
Db	2518	GGGTCTTCAAAAGTCAAGAAAGTAAAGCCATCATCTGCCTTTGATAGTAAAGAAAGAACNA	2577
QY	2563	aactgcggaaaagTccctatactcttaactgtaacTgaaaaaaTcccttccaacatTcaattat	2622
Db	2578	AATATCAAAACAATCCCAATCTTCACTGTAACGAAAGAAATCCCTCCAAATTCACATTTATTT	2637
QY	2623	gaacagctgtgtggaactgTgaagTgTccctccaaagaaacaaatctgcaatctgaagcTgc	2682
Db	2638	GAGCGATGTGGGGAGCTGGAATGGAATGCTCAAAAGGACTAGCTTGCATCTCAGCACTTCT	2697
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Db 2698 TTTCTCACCGGTTGCTCTTTTTCAGACACCTTTGGATTCCTCCGGCCACGCTCTTC 2757
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Qy 2803 ctggaacacacattatagataagataagataagataagataagataagataagataagata 2862
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RESULT 2
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LOCUS mouse msio mRNA, complete cds.
DEFINITION L16912 GI:347143
ACCESSION L16912.1
VERSION 1
KEYWORDS
SOURCE Mus musculus
ORGANISM Mus musculus adult brain cDNA to mRNA.
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 3591)
AUTHORS Butler, A., Tsunoda, S., McCobb, D. P., Wei, A. and Salkoff, L.
TITLE msio, a complex mouse gene encoding 'maxi' calcium-activated potassium channels
JOURNAL Science 261, 221-224 (1993)
MEDLINE 93318148
FEATURES
Source Location/Qualifiers
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BASE COUNT 946 a 917 c 843 g 885 t
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Query Match 21.2% Score 705; DB 94; Length 3591;
Best Local Similarity 54.8%; Pred. No. 3.2e-188;
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Qy 273 agaattgtgtcttcagaccagaccttgytgggaagtgtgtgacccctgtcttctgt 332
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3110 taacctt 3116
3248 TGCACTT 3254

RESULT 3
AF026001 3456 bp mRNA PRI 13-DEC-1997
LOCUS
DEFINITION Macaca mulatta calcium-activated potassium channel alpha subunit

mRNA, complete cds.
 AF026001
 AF026001.1 GI:2570857
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 rhesus monkey.
 Macaca mulatta
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 Cercopithecinae; Macaca.
 1 (bases 1 to 3456)
 Rae, J.L. and Shepard, A.R.
 REFERENCE
 Direct Submission
 TITLE
 JOURNAL
 Submitted (22-SEP-1997) Physiology and Biophysics, Mayo Foundation,
 200 1st Street SW, Rochester, MN 55905, USA
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 location/Qualifiers
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Query Match	21.2%;	Score 704.2;	DB 88;	Length 3456;
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 Db 422 TGAATGATATTCGCCCCAGACACTGACTGGCAGAGCTCGTGGTGTATGATCTTGGCTCA 481
 OY 338 gcaattgggtctctataatctatctatcaaatctgcgcagcccgcttgaagctc---tc 394
 Db 482 GCATTCGGTGCACCTTGATATTAATCTTCATAGATTGGTCAACCCATATGAATCGCCAGA 541
 OY 395 catcataatgaagaacaaaccactccatattgatttgggttttcaatgctctttagttcc 454
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OY	455	atttggatgaagtttaattgagcgcgaibacaaagaatcaatttcggcgtggaggaat	514
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OY	515	caatcgttagacatctttaccatcccaaccaaccttattctctattatttgaagagcaat	574
Db	662	CTGATAGGGAATTTCTTCAAGCGTGCCGCTGTTTGTGTCGTGATCTTAACACAGAT	721
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Db	782	TTCTGAATATTCTTTAAACAAGTAATTTCCATCAAGCTGGTGATCTGCTCTCCATATT	841
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Db	842	TCACACAGTGCGCTGACGTGCGAGCCGGGTTCATCCATTGGTGGAGAAATTACGGAGCCCAT	901
OY	755	ggctcaaaagtagaaattcaagaataatcatattttagtcaaatctaaccttgatc	814
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OY	995	agttattatgtgtcttgcgaacatcaacgttgaagcttgacgcgttcccggaagatt	1054
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Db	1562	CAATCTGCTTCGCAAGACTTAAGTTGGGCTTCAATACCCAGAGCTGCTCGCTCAAGGCC	1621
OY	1475	tgtgtaccttctaacaatctctatcttgttggagcaaaaacaaaggltatgcttaacaga	1534
Db	1622	TCTCTCACCATGCTTGGCAACCTCTTCTTCATGTAGGTCATTTAAAGATTTGAGAAACGA	1681
OY	1535	ccgtggaagaaaccttcttgaatagcatgaaaaaanaatcttgacccaagctctctg	1594

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Query Match	Best Local Similarity	Matches 1588; Conservative	21.2%; Score 704; DB 7; Length 3459; 55.0%; Pred. No. 6,1e-188; 1; Mismatches 1231; Indels 66; Gaps 8;
Oy	273	agaaatgttgccttcagccagacgcttcttgtagggaaggttgtagtcgataccttcttcttgc	332
Db	420	AGGGGTGATGATGATTCGCCGACGACTGACCGCGACAGATCGCTTGTTGCTTACGCTTTTGC	479
Oy	333	actaagcatctgggtcctctataatctatttcaatctcgtctgaacctgttgaagctg	392
Db	480	TCTCAGCAATTTGGTGACATGTTGTAATTAATCTTCTTCAATTCGTCGTAACCCAAATGAAATCTCG	539
Oy	393	---ttcatacatatgtaggaacaaacccattccattcttgatttgcttccaagcttcttcttgc	449
Db	540	CCAGATTTCTTCAACAAGATTTTCACATTCACAGATTCACATGACATGCGCTTTCACAGTGTCTTCC	599
Oy	450	ttctcatcttggatctgaagttctatctgacgctatctacaaagatcaagcttctgcttgaagat	509
Db	600	TCTCTACTTTGGCTTGCAGGCTTATTCGACGCCAACATGAAGCTGTGGTCTCGCTGGAAGT	659
Oy	510	gaattcaatcgttagacatccttaccatccaccacaaaccttattctctattatttgaagag	569
Db	660	GAACTCTGTAGTAGATTTCTTTCACGCGTCCCTCCGATATTTTGTTGTTGCTTACTTTAAACAG	719
Oy	570	caattgctcaggtttcaaggttccctaaagagccttgcgcctctgtagaactccctcaaatctt	629
Db	720	AAGTTGGCTTGGTTTGAAGCTTTTAAAGACTCTCAGACTGATCCAGATTTTTCAGAAATTTT	779
Oy	630	gcaaaattctacgagccatcaagaaccagtaactcagttgaagtttccaaactgctgtcaat	689
Db	780	GCAGTCTTCTGATATCTCCGTAAGAACAGTAATTCATCAAGCTGTGTGAATCTGCTCTCCAT	839
Oy	690	aattctagttacccttggttcaacagcgtcggtggtattcaatccctgtgtggaataatctcgtgga	749
Db	840	ATTATTCACGACATGCGCTGACAGCGCGGGTTCATTCATTTTGGTGGAGCCCTTCAGGGGA	899
Oy	750	tcacctggtctcaaaagtagaaattccagaatatacatataattttagtgtaattctaccgtgt	809
Db	900	CCCATGGGAAATTTCCAAACACACAGGCTCTCACCTACCTGGGAATGTGTACTTCTGCT	959
Oy	810	catggcaacacgtcaaccgtttgatttggagatgttggtagcgaagacatctttagagac	869

D	b	960	CATGGTACCATGTCCACTCTGGGTTATGTAGAGTGTTTTGTGAAAACACACTCTGGGGC	1013
Q	y	870	gaacccaacagtcctcctcaactcgggagttgatataatttcgcaactalatacctcga	929
D	b	1020	CCCTTCATAGGTCTTCTTCATCTCCGGGGAGCTGGCCATGTTTGGCAGCTACGTCTCTGA	1079
Q	y	930	aatgctggaaactcttcgtcctcaagaaggaaataaccagcttcmcttgaagacccaagaag	989
D	b	1080	AATATATGAGCTTAATATAGAAACCCGACAGAAATATCGGGGGCTCTTATAGTCCGTTAGTGG	1138
Q	y	990	aaagaattcatctatgctgctcgtgynaacaalcatcgtgcgaagtgfcagccgtcttcctga	1049
D	b	1140	AAGAAACACATTTGTGGCTGTGGACACATCATCTGTGGAGACGTTTCCAACTTCTTAA	1199
Q	y	1050	gaattcctccggagcaagtcgagaaagatcaaacctgtaattgtttcctcggagaaac	1109
D	b	1200	GGACTTCTTCTCACAGAGACCGGACGACGTCGAAGTGTCTTCTTCACACAT	1259
Q	y	1110	ccccctctcttggaacttgaaacccaattataatgctactcgtgcacacaagctcat	1169
D	b	1260	TTCCCTTAACCTGGAGCTTGAAGCTCTGTGTTCAAGACATTTTACTCAGGTGGATTTTA	1319
Q	y	1170	tctcgaatcgcgaatgaatgaggaagatctgagagagctggtggtggaatctgcagagc	1229
D	b	1320	TCAGGGTTCAGTCCCTTAATCCACATATCTTTCGAAGTCAAGATATGATGTCGACGATGC	1379
Q	y	1230	atgcctattatagccaatccctctgfcagtgatltcccaagcttgagaatatttccaacat	1289
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Q	y	1350	gcaatcccaacaagaagttatctgcgaagaagatctccagctggaactggaacccggagga	1409
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Q	y	1590	ctctgtagaacttgctcggaaatgaagctctcccgaaagttgcggcgctcgtcttcgaaga	1649
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Q	y	1830	gttcattctcgaagctaatcaacaactgctgcgcgaagaacagaaacgagcagacatcac	1889
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 DEFINITION Homo sapiens BKCA alpha subunit mRNA, complete cds.
 ACCESSION AF118141
 VERSION AF118141.1 GI:4868123
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE
 AUTHORS Cairns,V.R., Aebly,M.R. and Rusch,N.J.
 TITLE Cloning and Characterization of BKCA Alpha Subunit from Human Pulmonary Artery
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 3364)
 AUTHORS Cairns,V.R., Aebly,M.R. and Rusch,N.J.
 TITLE Direct Submission
 JOURNAL Submitted (04-JAN-1999) Physiology, Medical College of Wisconsin, 8701 Watertown Plank Rd, Milwaukee, WI 53226, USA

FEATURES
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CDS
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 BASE COUNT
 ORIGIN

Query Match 21.0%; Score 697.8; DB 89; Length 3364;
 Best Local Similarity 54.7%; Pred. No. 3.5e-186;
 Matches 1576; Conservative 1; Mismatches 1238; Indels 66; Gaps 7;

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RESULT 6
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LOCUS Human calcium-activated potassium channel (hslo) mRNA, complete cds.
DEFINITION
ACCESSION U23767
VERSION U23767.1 GI:758790
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 3537)
AUTHORS McCobb,D.P., Fowler,N.L., Featherstone,T., Linggle,C.J., Salto,M., Krause,J.E. and Salikoff,L.
TITLE A human calcium-activated potassium channel gene expressed in vascular smooth muscle
JOURNAL Am. J. Physiol. 269 (3 Pt 2), H767-H777 (1995)
MEDLINE 96024676
REFERENCE 2 (bases 1 to 3537)
AUTHORS Salikoff,L.

TITLE Direct Submission
JOURNAL Submitted (28-MAR-1995) Larry Salikoff, Anatomy and Neurobiology, Washington University School Medicine, 660 S. Euclid Ave., St. Louis, MO 63110, USA
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BASE COUNT 883 a 916 c 866 g 872 t
ORIGIN

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Best Local Similarity 54.7%; Pred. No. 3.5e-186;
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DEFINITION Homo sapiens large conductance calcium- and voltage-dependent
potassium channel alpha subunit (Maxik) mRNA, complete cds.
VERSION U11058.2 GI:7914977
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 5829)
AUTHORS Wallner,M., Meera,P., Ottolia,M., Kaczorowski,G.J., Latorre,R.,
Garcia,M.L., Stefani,E. and Toro,L.
TITLE Characterization of and modulation by a beta-subunit of a human
maxi Kca channel cloned from myometrium
JOURNAL 96419007
MEDLINE 8821792
PUBMED
REFERENCE 2 (bases 1 to 5829)
AUTHORS Wallner,M., Meera,P. and Toro,L.
TITLE Determinant for beta-subunit regulation in high-conductance
voltage-activated and Ca(2+)-sensitive K+ channels: an additional
transmembrane region at the N terminus
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 93 (25), 14922-14927 (1996)
MEDLINE 97121491
PUBMED 8962157
REFERENCE 3 (bases 1 to 5829)
AUTHORS Meera,P., Wallner,M., Song,M. and Toro,L.
TITLE Large conductance voltage- and calcium-dependent K+ channel, a
distinct member of voltage-dependent ion channels with seven
N-terminal transmembrane segments (S0-S6), an extracellular N
terminus, and an intracellular (S9-S10) C terminus
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 94 (25), 14066-14071 (1997)
MEDLINE 96054361
PUBMED 9391153
REFERENCE 4 (bases 1 to 3987)
AUTHORS Wallner,M.
TITLE Direct Submission
JOURNAL Submitted (21-JUN-1994) Molecular Physiology and Biophysics, Baylor
College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
REFERENCE 5 (bases 1 to 5829)

AUTHORS Wallner,M.
TITLE Direct Submission
JOURNAL Submitted (17-MAY-2000) Department of Anesthesiology, University of
California Los Angeles, Los Angeles, CA 90095-7115, USA
REMARK Sequence update by submitter
COMMENT On May 17, 2000 this sequence version replaced gi:507921.
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RESULT 8
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 LOCUS AF036626 3581 bp mRNA VRT 18-MAY-1998
 DEFINITION Trachemys scripta calcarata activated potassium channel mRNA,
 alternatively spliced thc3 isoform, complete cds.

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ACCESSION AF036626
VERSION AF036626.1
KEYWORDS GI:3136119
SOURCE red-eared slider turtle.
ORGANISM Trachemys scripta
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REFERENCE 1 (bases 1 to 3581)
          Jones, E.M., Laus, C. and Fettiplace, R.
          Their distribution in the turtle cochlea
          Proc. R. Soc. Lond., B, Biol. Sci. 265 (1997), 685-692 (1998)
JOURNAL 98271655
MEDLINE 2 (bases 1 to 3581)
REFERENCE Jones, E.M., Laus, C. and Fettiplace, R.
          Direct Submission
          Submitted (04-DEC-1997) Physiology, University of Wisconsin-
          Madison, 1300 University Ave., Madison, WI 53706, USA
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REFERENCE			
AUTHORS			1 (bases 1 to 3769)
			Tseng-Crank,J., Foster,C.D., Krause,J.D., Mertz,R., Godinot,N.,
			D'Clhara,T.J., and Reinhardt,P.H.
			Cloning, expression, and distribution of functionally distinct
			Ca(2+)-activated K+ channel isoforms from human brain
			Neuron 13 (6), 1315-1330 (1994)
JOURNAL			
MEDLINE			95085775
REFERENCE			2 (bases 1 to 3769)
AUTHORS			Tseng-Crank,J.
TITLE			Direct Submmission
JOURNAL			Submitted (30-JUN-1994) Julie Tseng-Crank, Molecular Genetics,
			Glaxo Research Institute, 5 Moore Drive, Research Triangle Park,
			27709, USA
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[illegible]

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Matches 1575; Conservative	1; Mismatches 1239; Indels 66; Gaps 7;				
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RESULT 11
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LOCUS HSU13913 4149 bp mRNA PRI 05-JAN-1996
DEFINITION Human large-conductance calcium-activated potassium channel (hsl10)
ACCESSION U13913
VERSION U13913.1 GI:537438
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 79 to 3615)
REFERENCE
AUTHORS Dworetzky,S.I., trojnakl,J.T. and Gribkoff,V.K.

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TITLE      Cloning and expression of a human large-conductance
JOURNAL    calcium-activated potassium channel
MEDLINE    Brain Res. Mol. Brain Res. 27 (1), 189-193 (1994)
REFERENCE  95182815
AUTHORS    Butler, A., Tsunoda, S., McCobb, D. P., Wei, A. and Salkoff, L.
TITLE      2 (sites)
JOURNAL    mslo, a complex mouse gene encoding 'maxi' calcium-activated
MEDLINE    potassium channels
REFERENCE  Science 261 (5118), 221-224 (1993)
AUTHORS    93318148
TITLE      3 (bases 1 to 4149)
JOURNAL    Dworetzky, S.
REFERENCE  Direct Submision
AUTHORS    Submitted (23-AUG-1994) Steven Dworetzky, Neurodegenerative
TITLE      Disorders/405, Bristol-Myers, Squibb Company, 5 Research Parkway,
JOURNAL    Wallingford, CT 06492-7660, USA
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Query Match 21.0%; Score 696.2; DB 97; Length 4149;
Best Local Similarity 54.7%; Pred. No. 1e-185;
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ORIGIN

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Oy	630	gcaaatcttcagagccatcaagaacagcatcaacagctgaagtttccaacatcgttcaat	689		
Dd	779	GCAGTTTCTGAAATNCTTTAAAAACAAGTAAATTCATCAAGCTGGTGAATCTCTCTCCAT	838		
Oy	690	aattcctcagtacctgtgttcaacagctgcggatcatlcaacctgttgaagaaattctgttga	749		
Dd	839	ATTATATCAACACAGTGGCTGACAGCTGAGCTGATATCCACTTGGTGGAGAAATTCAGGGGA	898		
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TITLE	Molecular biology and electrophysiology of calcium-activated potassium channels from lens epithelium		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 3414)		
AUTHORS	Rae,J.L. and Shepard,A.R.		
TITLE	Direct Submersion		
JOURNAL	Submitted (27-AUG-1998) Physiology, Mayo Foundation, 200 1st Street SW, Rochester, MN 55905, USA		
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 Jjiang,G.-J., Zidanic,M., Michaels,R.L., Griguer,C. and
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 CS10 encodes calcium-activated potassium channels in the chick's
 cochlea

JOURNAL Proc. R. Soc. Lond., B, Biol. Sci. 264 (1382), 731-737 (1997)
 MEDLINE 97321842
 REFERENCE 2 (bases 1 to 3968)
 AUTHORS Jjiang,G.-J., Zidanic,M., Griguer,C. and Fuchs,P.
 TITLE Direct Submission
 JOURNAL Submitted (30-MAR-1995) Paul Fuchs, Physiology, University of
 Colorado Health Sciences Center, 4200 E. Ninth Ave. #C240, Denver,
 CO 80262, USA

FEATURES
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